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Aegilops tauschii
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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Pooideae, Triticeae, Aegilops.
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Sequence 10 from Patent WO9914314.
AX031271 1 GI:10278603
Li,Z., Morell,M. and Rahman,S. Regulation of gene expression in plants
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Qy 301 CTCCCCGTCTGGCTTTGGCTTCCCCTTCTCTCTGCGCGCGCATGGCCTTTCATT	JOURNAL Patent: NO 9914314-A 10 25-MAR-1999; GOODMAN FIELDER LTD (AU); LI ZHONGYI (AU); MORELL MATTHEW (AU); RAHMAN SADEQUR (AU); UNIV AUSTRALIAN (AU); COMMW SCIENT IND RES ORG (AU); GROUDE LIMAGRAIN PACIFIC PTY L (AU) FEATURES SOURCE (AU); GROUDE LIMAGRAIN PACIFIC PTY L (AU) LOCALION/QUALIFICERS (AU); COMMW SCIENT IND RES ORG (AU); GROUDE LIMAGRAIN PACIFIC PTY L (AU) LOCALION/QUALIFICERS (AU); COMMW SCIENT IND RES ORG (AU); GROUDE LIMAGRAIN PACIFIC PTY L (AU) LOCALING MARCH (AU); COMMW SCIENT IND RES (AU); COMMW SCIENT IND RES (AU); COMMW SCIENT IND RES (AU); COMMW SCIENT IND RES (AU); CROMEN IND (AU)
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Qy 720 CGGTAAATCTTCATACAATCGTTATTCACTTACCAAATGCCGGATGAAACCAACC		
Qy 661 AGAG-GACGACTIGGCAAGTCCGGCGCAACTCCTGAAGAATTACAGGTACACACTCGTGC 1777 Db 1718 AGAGCGACGACTTGGCAAGTCCGGCGCAACCTGGAAGAATTACAGGTACACACAC	537,67396867, 939,1011610193,	
1658	join (1204. 1336, 1664. 1761.2038. 2279, 2681. 2779, 2681. 2799, 2681. 2799, 2681. 2799, 2681. 2949. 2991, 3144. 3203, 3539. 3619, 3703. 3819, 4105. 4188, 2949. 2991, 3144. 3203, 3539. 3619, 3703. 3819, 4105.	CDS
CGTCCTGAGCCGCGGCGCCTCTCCAGGGAAGGTCCTGGTGCCTGACGGCG	939,1011610193,	
Qy 541 CTGTTCTTGCTGTAACTGCAAGTTGTGGCGTTTTTCACTATTGTAGTCATCCATC	1336,16641761,20382279,26812779, 1443203,35393619,37033819,41054188, 1155234,62096338,64276537,67396867,	mRN
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421 CTGAACCTGTATTTTTTCCCCCGGGGGAAATGCGTTAGTGTCACCCAGGCCCTGGTGTT	AL Submitted (18-JAN-2001) Plant Industry, CSIRO, Clunies Ross, Camberra, ACT 2601, Australia	JOURNAL
1418 GCTGTTCCCCAATTGATCTCCATGAGTGAGAGATAGCTGGATTAGGCGATCGCGCTTC	11244112 2 (bases 1 to 11475) Rahman,S., Regina,A., Li,Z., Sharon,A. and Morell,M.K.	REFERENCE AUTHORS
361 GCTGTTCCCCAATTGATCTCCATGAGTGAGAGAGATAGCTGGATTAGGCGATCGCGCTTC	י אי	JOURNAL
	enzyme IIa from the wheat genome donor Aegilops	
1298 ACTTGCCGTGCTGCTCCTCAGGAAGAAGGACTCCTCTCGTACGCCTCGCTCTCGAAT	Kosar-Hashemi, Comparison of relationships	TITLE
7 241 ACTTGCCGTCGCTCCTCAGGAAGAAGGACTCCTCTCGCTACGCCTCGCCTCTCTCGAAT 300	1 (bases 1 to 11475) Rahman, S., Regina, A., Li, Z.,	REFERENCE AUTHORS
181 GTGTGGCGCGGGCGGCGGCGGCCGGCCCGCCTCGGAGCGGAGGGGCGGGC	Eukaryota Spermatop Pooideae;	
1178	Aegilops tauschii SM Aegilops tauschii	SOURCE ORGANISM
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/gene="SDella" exon	/product="gtearch branching enzyme IIa" /product="gtearch branching enzyme IIa" /protein_id="AAC72335.1" /db_xref="Gt:3851526" /translation="MAEVNMTGGAAEKLESSEPTQGIAETITDGVTKGVKELVVGEKP /translation="MAEVNMTGGAAEKLESSEYK" QVVPKCGDGQKIYEIDFTLKDFRSHLDYRYSEYK" intron 14351836	/gene="sbella" /number=1 join(12171434,1837>1852) /gene="sbella" /gene="sbella" /EC number="2.4.1.18"	mRNA join(7641434,1837>1852) /gene="sbeIIa" /product="starch branching enzyme IIa" exon /641434	CAAT_signal 719722 TATA_signal 727730 /gene="sbella"	gene /gene="sbella" CAAT_signal 706709 /gene="sbella"	DNA"	Stockholm : Lockholm : 1	REFERENCE 2 (bases 1 to 1852) AUTHORS Sun,C., Sathish,P., Ahlandsberg,S. and Jansson,C. TITLE Direct Submission JOURNAL Submitted (11-MAY-1998) Stockholm University, Biochemistry,	differentially expressed in barley Plant Physiol. 118 (1), 37-49 (1998) 9804232 9733524	Pooldeae; Triticeae; Hordeum. REFERENCE 1 (bases 1 to 1852) AUTHORS Sun,C., Sathish,P., Ahlandsberg,S. and Jansson,C. The two cease acceding starch branching environs IIa and IIh are	Hordeum vu M Hordeum vu Eukaryota; Spermatoph	gene, nuclear gene encoding plastid protein, partial cds. AF064562.1 GI:3851525	RESULT 3 AF064562 AF064562 AF064562 AF064562 AF064562 AF064562 AF064562 AF064562 AF064562	157 TAGGTGACTTCAACAATTGGAATCCAAATGCAGATACTATGACCAGAG	3097 GACC	QY 1980 GTTAATGGTCACTATTCACCAACTAGCTTACTGGACTTACAAATTAGCTTACTGAATACT 2039

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Best Local Similarity 87.6
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                                                               TGGGCCACTGAAAAAATCAGATGGATGTGCATTCTAGCAAGAACTTCACAACATAATGCA
                                                                                                                                                                                                                                    TTACCAAATGTCGGATGAAACCAAGCCGCAGAGGCGTCAGGTTTCAAGCTTCTTCTATCA
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Pred. No. 2.7e-281;
1; Mismatches 168;
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Best Local Similarity 98.0
Matches 246; Conservative
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          978 AGATACCTGAAGATATCGAGGAGCAAACGGCGGAAGTGAACATGACAGGGGGGACTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                               AR340173
Sequence
AR340173
                                                                                                                                                                                         1 (bases 1 to 2853)
Willmitter,L., Kroger,C., Lutticke,S. and Lorz,H.
Nuclectide sequences encoding enzymes that alter of concentration and composition in plants
Patent: US 6570066-A 3 27-MAY-2003;
Location/Qualifiers
1. 2853
                                                                                                                                                                                                                                                                                                                                             Unclassified.
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/mol_type="genomic
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patent US 6570066.
                                                    Score 243; DB 6; Pred. No. 4.6e-48; 0; Mismatches 5;
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Best Local Similarity 98.0%;
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6-alpha-D-(1,4-alpha-D-glucanotransferase
U66376
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                             Kroeger, C., Loerz
Direct Submission
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                                                                                        GI:1620661
                                                        WIDFFEGPOTLPTGKYLPGNNNNYDKCRRRFDLGDAEFLRYRGMQEFDQAMQHLEEKY
GFMTSEHQYVSRKHEEDKVIIFERGDLVFVFNFHWSNSFFDYRVGCSKPGKYKVALDS
DDALFGGFSRLDHDVDYFTTEHPHDNRPRSFSVYTPSRTAVVYALTE"
                                                                                                                                                                                                                                                                                                       Organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="T.A. Florida"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                       tissue_type="kernels 21313. .2502
                                                                                                                                                                                                                                                   codon_start=1
                                                                                                                                                                                                                                                           note="branching enzyme"
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                                                                                                                                                                                                                                                                        _number="2.4.1.18"
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 Score 243; DB 8; Length 2853; Pred. No. 4.6e-48; 0; Mismatches 5; Indels
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                            ACCEGTAATEC 1228
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Query Match
Best Local Similarity
Matches 243; Conserv
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FLI_CDNA.
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1 (bases 1 to 2549)
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Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours a Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tingey,S.V., Wolters,P., Powell,W., Dolan, Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
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                      ATGGGCAGAAAATATACGAGATTGACCCAACACTGAAAGATTTTCGGAGCCATCTTGACT
                                                                           CCAAAGGAGTTAAGGAACTAGTCGCGGGGGAAAACCGCGAGTTGTCCCCAAAACCAGGAG
ATGGGCAGAAATATACGAGATTGACCCAACGCTGAAAGATTTTCGGAGCCATCTTGACT
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j. .2549
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Triticum aestivum"
/mol type="mRNA"
/db_xref="taxon:4565"
/clone="wde1f.pk002.g8:fis"
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Pred. No. 6.7e-47;
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, full insert mRNA
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Matches 241; Conserv
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Triticum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rahman,S., Regina,A., Li,Z., Mukai,Y., Yamamoto,M., Kosar-Hashemi,B., Abrahams,S. and Morell,M.K.
Comparison of starch-branching enzyme genes reveals evolutionary relationships among isoforms. Characterization of a gene for starch-branching enzyme IIa from the wheat genome donor Aegilops
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 2726)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21140316
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ATGGGCAGAAAATATACGAGATTGACCCAACACTGAAAGATTTTCGGAGCCATCTTGACT 1217
                                                                                                                                                               AGATACCTGAAGATATCGAGGAGCAAACCGGCGGAAGTGAACATGACAGGGGGGAACTGCAG 1037
                                                                CCAAAGGAGTTAAGGAACTAGTCGTGGGGGAGAAACCGCGAGTTGTCCCAAAACCAGGAG 1157
                                                                                               AAAAACTTGAATCTTCAGAACCGACTCAAGGCATTGTGGAAACAATCACTGATGGTGTAA 319
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|mol_type="mRNA"
                                                                                                                                                                                                                                              10.9%;
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                                                                                                                                                                                                                                              Score 235; DB 8;
Pred. No. 4.1e-46;
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mat_peptide

gene="sbe2"

polyA_signal

/product="1,4-alpha-glucan branching enzyme
/EC_number="2.4.1.18"

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Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nair,R.B., Baga,M., Scoles,G.J., Kartha,K.K. and Chibbar,R.N. Isolation, characterization and expression analysis of a starch branching enzyme II cDNA from wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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                                                                                                                                                        /db_xref="Goreval"
/db_xref="del"
/db_xref="Goreval"
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PHDNRPRSFSVYTPSRTAVVYALTE"
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/protein_id="CAA72154.1"
/db_xref="G01:1885344"
/db_xref="GOA:P93691"
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/EC_number="2
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151. .2622
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gene="sbe2"
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McCue, K.F., Hurkman, W.J., Tanaka, C.K. and Anderson, O.D. starch Branching Enzymes Sbel and Sbe2 from Wheat (Triticum aestivum cv. Cheyenne): Molecular Characterization, Developm Expression, and Homolog Assignment by Diffferential PCR plant Mol. Rep. 20 (2), 191-192 (2002)

C (bases 1 to 2970)

McCue, K.F. and Anderson, O.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF286319 2970 bp mRNA linear PLN 14-MAR-2003
Triticum aestivum starch branching enzyme 2 (Sbe2) mRNA, complete
                                                                                                                                                                                                                                                               Submitted (11-JUL-2000) United Agricultural Research Service, 94710-1105, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triticum aestivum (bread wheat)
Triticum aestivum
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AF286319.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pooideae;
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                                                                                                                                                                                                                                                                                                                  rect Submission
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2948
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2930. .2935
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                          /gene="Sbe2"
/EC number="2.4.1.81"
/note="glucosyltransferase; alpha-1,4-glucan;
/_alpha-1,4-glucan-6-glucosyltransferase"
                                                                                             /gene="Sbe2"
149. .2620
                                                                                                                              /tissue_type="endosperm"
|. .2970
                                                                                                                                                              cultivar="Cheyenne"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                              ocation/Qualifiers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triticeae; Triticum.
                                                                                                                                                                                                              organism="Triticum aestivum"
product="starch branching enzyme
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Pred. No. 4.2e-46;
0; Mismatches 10
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Varidiplantae; Streptophyta; Embryophyta; Poales; Poaceae;
                                                                                                                       98404232
9733524
                                                                                                                                                                                                                                                                                                                                                       Hordeum vulgare cultivar Bomi starch branching enzyme IIa (sbeIIa)
                                           Submitted (11-MAY-1998) Stockholm Stockholm S-10691, Sweden
                                                                                                                                                   Sun,C., Sathish,P., Ahlandsberg,S and J
The two genes encoding starch-branching
differentially expressed in barley
Plant Physiol. 118 (1), 37-49 (1998)
                                                                          2 (bases 1 to 2554)
Sun, C., Sathish, P., Ahlandsberg, S.
Direct Submission
                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; Pooideae; Triticeae; Hordeum. 1 (bases 1 to 2554)
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                              Location/Qualifiers
organism="Hordeum vulgare subsp. vulgare"
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Pred. No. 1e-45;
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                                                             University, Biochemistry,
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                                                                                             and Jansson, C
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/mol_type="mRNA"

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Best Local Similarity 93.0
Matches 211; Conservative
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                               Miao,H.M., Han,J.F. and Fleming,J.E. Direct Submission Submitted (31-JUL-2003) Institute of Biotechnology, Her of Agricultural Sciences, No.1 Nongye Road, Zhengzhou, Province 450002, China
                                                                                                                                                      1 (bases 1 to 3094)
Miao, H.M., Han, J.F. and Fleming, J.E.
Investigation of endosperm-specific promoters
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                      AY357072 3094 bp DNA linear I
Triticum aestivum cultivar Yumai-18 starch branching
(Sbella) gene, promoter region and partial cds.
                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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Triticum aestivum
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AY357072.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCAGGGTATTGCGGAAACAATCACTGATGGTGTAACCAAAGGAGTTAAAGAACTAGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCCAACGCTGAAAGATTTTCGGAGCCATCTTGACTACCGATACAGC 231
                                                                                                                                       (bases 1 to 3094)
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QVVPKPGDGGKIYELIVDFSKHLDYRYSEKAIRAALDQHEGGLEVFSRGYEEKG
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FTRSAKGITYREMAPGAHSAALVGDFNNMNPNADTMTRDDYGVWEIFFLANDGSPAI
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HVTNFFAPSSRRGTPEDLKSLINFADEVLLPRIKRLGYNAVQIMALQHSYYASFGV
HVTNFFAPSSRRGTPEDLKSLINFADEVLLPRIKRLGYNAVQIMALGHSYYASFGV
HVTNFFAPSSRRGTPEDLKSLINFADEVLRTLLSNARWHLESYXFDGFREPGGVTSMMYTHH
YFHGGFRHHMMDSRLFNYGSNEVLRFLLSNARWHLESYXFDGFREPGGVTSMMYTHH
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LEEKKGFMTSSHQYVSRKHEEDKVIIFERGDLVFVFNHEMSNSKKDYRVGCSKPGKYK
LEEKKGFMTSSHQYVSRKHEEDKVIIFERGDLVFVFNHEMDDGAALMINN EEG
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/product="starch branching enzyme IIa"
/protein_id="AAC69753.1"
/db_xref="GI:3822020"
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/db_xref="taxon:112509"
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/EC_number="2.
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                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                    GI:34329814
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    Fu,G., Wang,S.Y.,
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3066 CTGGCTGACTCAATCACTACGCGGGGATG 3094
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        Peng,Q., Zhang,Y., Hao,P., Wang,S., Fu,G., Huang,Y., Li,Y., Zhu,J., Liu,Y., Hu,X., Jia,P., Zhang,Y., Zhao,Q., Ying,K., Yu,S., Tang,Y., Weng,Q., Zhang,L., Lu,Y., Mu,J., Lu,Y., Zhang,L.S., Yu,Z., Fan,D., Li,Y., Li,T., Li,T., Hu,H., Guan,J., Wu,M., Zhang,R., Zhou,B., Chen,Z., Chen,L., Jin,Z., Wang,R., Yin,H., Cai,Z., Ren,S., Lv,G., Gu,W., Zhu,G., Tu,Y., Jia,J., Yin,H., Cai,Z., Kang,H., Chen,X., Shao,C., Sun,Y., Hu,Q., Zhang,Y., Chen,J., Kang,H., Chen,X., Shao,C., Sun,Y., Hu,Q., Zhang,X., Zhang,W., Wang,L., Ding,C., Sheng,H., Gu,J., Chen,S., Ni,L., Zhu,F., Chen,W., Lan,L., Lai,Y., Cheng,Z., Gu,M., Jiang,J., Li,J., Hong,G., Xue,Y. and Han,B.
Sequence and analysis of rice chromosome 4
                                                                                                                                                                                                                                                                                                                                                                    AL731641.3 GI:32490295
HTG; HTGS PHASE2.
Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSJN00286 159683 bp DNA linear HTG 14-NOV-20 Cryza sativa (japonica cultivar-group) chromosome 4 clone OSJNBa0042115, *** SEQUENCING IN PROGRESS ***, 11 ordered pieces. AL731641
Nature 420 (6913), 316-320 (2002)
                                                                                                                                                                                                                                                                                                                                                 Ehrhartoideae; Oryzeae; Oryza.
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/cultivar="Yumai-18"
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<1. .>3094
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/EC_number="2.4.1.81"
/note="glucosyltransferase"
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2684. .2689
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100.0%; Pr
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thes 0;
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Ren, S.X.,

Lv, G., Lin, W.,

Gu, W.Q.,

Zhu, G.F.,

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COMMENT
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* NOTE: This is a 'working draft' sequence. It currently * consists of 11 contigs. Gaps between the contigs * are represented as runs of N. The order of the pieces * is believed to be correct as given, however the sizes * of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bhan@ncgr ac.cn
Cryza sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC
clone: OSZNBA0042115.
On Jul 9, 2003 this sequence version replaced gi:21912624.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-MAY-2002) Han Bin, National Center for Gene Research, Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233, CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.ncgr.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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1 9353: contig of 9353 bp in length 9354 9553: gap of 200 bp 9554 47134: contig of 37581 bp in length 47315 51470: contig of 4136 bp in length 51471 51670: gap of 200 bp 51671 62557: contig of 1087 bp in length 62558 62757: gap of 200 bp 62758 82635: contig of 19878 bp in length 62758 82635: contig of 19878 bp in length 62758 82635: contig of 19878 bp in length 82636 82635: gap of 200 bp 82636 82635: gap of 200 bp 10 length 82636 82635: gap of 200 bp 10 length 82636 82635: gap of 200 bp 10 length 82631 102830: contig of 14091 bp in length 102631 102830: gap of 200 bp 102631 10283
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83
complement (2889...4076)
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complement (2889...4076)
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mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variety="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142542: contig (
142542: gap of 2
159683: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 bp
of 17141 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 6849 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEVARBYIRRAIRHLEKGRIVIFAGIGAGIGNDLFTTDTAAALRASELIANDVILKTT
AGDDDYGCPPRGNNNPPFEHISFRELAARGFSRMDMTAITCCQENNIPVVIFNMLEPG
NISKALCGDOYGTLVDQSGRITT
Complement (25712 . .27220)
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complement(join(25712 . .25917, 26704 . .27220))
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AGRRTPSKVLVSVAVORSLWPLHVMASAAWSVADLVAAAVALYVKEGRRPPLPSADPS
                                                                                                                                                                                                                                                                                                                                                                                           /gene="CSJNBa0042I15.5"
/codon start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13031. .14314
                                                                                                                                                                                                                                 /proteIn id="CAE04883.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                  )FGLHYSQFSLESLDPREKVMELGSRSFFLCPKSSAAVHAPSPSCSSDEASRIRDRDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MRPWERROVGAEGGESVGREDTDTNTNTTASSANASTSSSTAAS
GSSGARRNGAAAAAGEGWGRSSLSTATINLSOBYTLAHTSSYHEIWAKIHVDGGDGQ
REGGVGGGGGEDEDEDRCTLAGVLOPEDAVVERALGDAPDTELTRLAADYLRSTH
HASLLCLSIRRALKARARALVGDITDLLALIPHAPPLAAPHRDCAFDAFLLFDOMPNPF
PAPAAGFQGMHRSFVGKNHILDLRLLRARRRRLVRCATGASGICLIACATGAAIAGL
VLATHAITVLLAAAPACAASRGSCCPATASMKRLOQHMDRLDAARGAYLUNNDUDTI
ERLVGRLHATVESDKLLVRLGLISGRGCEHHTIESVVRQLRKNHPSLLRQLADLEEHIC
LYFAAVNRARLLIVNHLSAQSDPDRLSFHCHDIIQ"
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GSRYAVQRSGNILMAFNNKEASLAVPLFSPVIVPMAQSFGPIFSQLTSYPTLRFGVKS
YYGISRNLLIKFKDDQIDETSILAQVLSSESAISSLLDMSIRSLPGDHGLPLQOVLPD
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KQSREGWGSTGDWTEIEGAWVLKPKSQEPSFVVHFVGGIFVGAAPQITYRFFILERLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (join(7405. .7638,7818. .7988,9896. .1003, 10856. .1091,11192. .11255,1329. .11437,11951. .120,11175. .12244,12325. .12611))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(20187. .20980,21068. .21212,21288. .21341,21428. .21519,
22360. .22595,22729. .22902,22994. .23091)
/gene="OSUNBa0042I15.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPPAMADAVNRGGELLTNILATGTPWEAVAKEVGSTLGADSGVLRAQISKDVNTLVDVI
VSWIESNSGPRLLRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (7405. .12611)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13031. .14314
/gene="OSJNBa0042I15.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="OSJNBa0042115.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="OSJNBa0042115.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein_id="CAE04881.2"
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Matches 722;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATCATTCCTCGTTTCATTCTGATATATATTTTCTCATTCTTTTTTTCTTCCTGTTCTTGCT
TGAACATGACAGGGGGGACTGCAGAGAAACTTCAATCTTCAGAACCGACTCAGGGCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTTTTCTTGCCGGATAAGATGAGTTAGTGTTACAAATCGCTGTGATCATTCTCTAATTC
                                                                                                                                                                                                                                                                                                                                           TTCATTTTGTTAGCCTTGGCCCCGTGCTGGCTCTTGGGCCACTGAAAAATCAGATGGAT
                                                                                                                                                                                                                                                                                                                                                                                                  TAGTGGCAATGCCAGGTT----TCATGTGTTTTGTGCATTGTGACCTTGTGCTGGCTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGCCGGGAATÄÄAATTCGAGCTGTTGTCATTCACTGACCAAATGTGTGATGAAATGATG 125533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGTGGGGGTGGTATGGCGTTGCCTGACTAGTAGAGTCGGCTTTGCA-TTTGCAGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTAACTGCAAGTTGTGGCGTTTTTTCACTATTGTAGTCATCCTTGCATTTTTGCAGGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGÁTAATAAÁGTAAAACCTTTTTGÁGGAGGAGGÁÁGAGÁTTCCAG----CÁGTGGCAGAAG
                                                                                                                                                                                      TTTTTTCTTTTTGGGTGTCTCATGCAGAGTCTATCCATCTATGTTCTGTGTAGATACCTG
                                                                                                                                                                                                                                         GTGCATTCTAGCAAGAACTTCACAACATAATGCACCGTTTGGGGGTTTCGTCAGTCTGCTC
                                                                                                                                                                                                                                                                                          GGCTACTGAAAACCAAGTTGGGTCTTCCAACTAGCAACTTTGCCACAAAAGAATGTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACGGATGCGTCAGGTTTCGAGCTTCTTCTATCAGCATTGTGCAGTACTGCACTGCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGCTGTCCTCTGCGGAACCAGACGTGGAAACTCAAGAGCAACCTGAAGAATCTCAGGTA 125593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCCTGAGCCGCGCCGCCTCTCCAGGGAAGGTCCTGGTGCCTGACGGCGAGAG-GACGAC
                                                                                                                                  TACAATTGCTATTTTCGTGCTGTAGATACCTGAAGATATCGAGGAGCAAACGGCGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTCCCCCGCGGGAAATGCGTTAGTGTCACCCAGGCCCTGGTGTTACCACGGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - GGTAAATCTTCATACAATCGTTATTCACTTACCAAATGCCGGATGAAACCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDSSDEESDNELDDVLKSFSKPAMQHLAKLMRALDTLKKENERLIGTLVKYGCMKTYHS
KDALYKTITAHENKOGHGLGFSSES PVSKRVMYMGKECLMFVREESKVVAXFNGDYNK
EYHTCYWPKALAYSYDGOSSWYVDSGCTNHMTGERSMFTSLDEKGGSRENIVFGDDGK
EKLQFIIRVSIVRDDSSIAFKGVLKGDLYLVDFDVDRVNPEACLIAKSSMGWLWHRRL
AHVGNENLASLLKGEHLIGLSNVSFEMDRVCSACQAGKQVGSPHPIKNIMTTTRFLEL
LHMDLFGPVAYISIGGNKYGFVIVDDFSCFTWYFLHDKSACADDVFKRFTLIEAARAM
LDEYKTSDNGGEFKNTQVEEFLDEEGIKHEFSAFYDPRQNIVSYFRVEGKFFD
LTIKKVRSDNGGEFKNTQVEFLDEKGIKHEFSAFYDPRQNIVSYFRVEGKFFT
LDEYKTSDVFYAAEAVSTACHAINRLYLHKILKKTSYELLSKKKNVSYFRVEGKFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MKLHLISLHPSIWKVVCTGVDVPHDDMELTSEQEQLIHRNAQAS NAILSTLSELEENKVDGLEEAKBICDTLQLAHEGSPAVBAKIELLEGRLGEFVNDDK ETPQEMYDRMMILVNKIKGLGSEDMTNHFVVRAKLLREFGPRNPTLVSMIREKKDFKRLTLSDLIGRIVSHEMQSEBEARKTBRRVKAFKHFLAKSGYGKGRKDDDXGKKQSKRACFN CGEYGHFIADFFKSNEAKAGGKKXPERAHVABAHMPEVWYSGDEEDFEVKPKPKPKDKDKDGEGGVATVTFKSSSSSKERLFNNLSDDDDDSYHYSCFMAQGRKVMTQKPSHTSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (47475. .52886)
/gene="CSJNBa0042115.6"
complement(join(47475. .49504,49559. .50502,50555.
complement(join(47475. .49504,49559. .50502,50555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNLRTSGSEDVPTAQVDGIDAAGTLGHTDQAQVPLVHHPRIHHTVQRDHPVDNILGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSKMPRSSKFSPKVDEGFLLGYESNAHAYRVFNKTSGEQVVIHVVRDVDPSQAIGTKA
IGDIRPVETQDDQEDRDQPPSSTSNSPTSVVSAEPEVPGPIDRNLRTSPGPEVPGSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein_id="CAE04884.2"

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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.6%;
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Pred. No. 2e-22
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .8;
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Oryza sativa
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryzea.

CE 1 (bases 1 to 3015)

I (bases 1 to 3015)

NEW RICE GENE FOR STARCH-BRANCHING ENZYME

NEW RICE GENE FOR STARCH-BRANCHING ENZYME

NITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK, MITSUI PETROCHEM IND LTD

OS Oryza sativa (rice)

PN 1998004970-A/1

PD 13-JAN-1998

PF 24-JUN-1996 JP 1996162983

PF 24-JUN-1996 JP 1996162983
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E14723.1 GI:5709406
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E BABA TANADASHI, KAWASAKI TSUTOMU, ICHIKAWA NORIO PC

BABA TANASHI, KAWASAKI TSUTOMU, ICHIKAWA NORIO PC

12N15/09, A01H5/00, C07H21/04, C12N5/10, C12N9/10, (C12N15/09,
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/mol_type="genomic DNA"
/db_xref="taxon:4530"
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/cultivar='Nihonbare'
/clone_lib='Rise Immature
,...ibrary'
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Pred. No. 7e-22;
0; Mismatches 52;
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/clone='pRB41'
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KEYWORDS
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ORGANISM
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Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                  AB023498
Oryza sativa mRNA for starch
                                                                                                          2 (bases 1 to 3015)
Mizuno,K. and Baba,T.
Direct Submission
Submitted (09-FEB-1999) Kouichi Mizuno,
Institute of Agricultural and Forest Eng
Tsukuba, Ibaraki 305-8572, Japan
                                                                                                                                                                                                                     Mizumo,K., Tachibana,M., Kobayashi,E., Kawasaki,T., Funane,K., Kobayashi,M. and Baba,T.
Kobayashi,M. and Baba,T.
Molecular cloning and expression analysis of a novel member of starch branching enzyme isoform in developing rice seeds
                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                     starch branching enzyme rbe4.
                                                                                                                                                                                                                                                                                                                                                                                     AB023498.1 GI:5689137
                                                                                 Fax:81-298-55-2203
                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                   starch branching enzyme
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                                                                                             (E-mail:koumno@sakura.cc.tsukuba.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGACATTGAGGAAAATGTGACTGAGGGTGTGATCAAAGATGCTGATGAACCAACTGTGGA 568
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76.3%;
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/clone='pRB41'
129. 2654
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Pred. No. 7.5e-22;
0; Mismatches 52;
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branching 6
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                                                                                                                            no, University of Tsukuba,
Engineering; 1-1-1 Tennoudai,
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                                                                                                  Tel:81-298-53-4656
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Search completed: April 10, 2004, 10:02:19 Job time: 8425.29 secs
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Best Local Similarity
Matches 167; Conserv
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/translation="mAsfaVvSGARLGVVRAGGGGGGGGGGARRSGGYDLPSVRVPBDDQQ
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ALIGNMENTS

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RESULT 1
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05-JUL-1999
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                                                                                                                                                                                                                         New isolated cereal plant enzyme genes used for, antisense sequences of granule bound synthase.
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20-MAR-1998;
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The invention relates to a novel enzyme of starch biosynthetic pathway in a cereal plant, where the enzyme is selected from starch branching enzyme (SBE) I , SBE II, starch soluble synthase (SSS) I, and debranching enzyme (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of

Claim 8; Page 75-81; 171pp; English.

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601 TIGCAGGGCCCGTCCTGAGGCCGCGCCCTCCAGGGAAGTCCTGCTCCTGATGCACGGCCGTCCTGAGGCCGCCGCCCTCCAGGGAAGGTCCTGGTGCCTGAGGCGCGCGC	78 cigaaccigiairitiiicccccicicicicaaaaiacciiiaaiaiacigicaccaaiaccigiii 1 81 accacagactigataataataataataataatatatatatatatatata	1358 CTCCCCCGTCTGGCTTTGGCTCCCCTTCTTCTCTCTCTGCGCGCGCATGGCCCTGTTCGAT 1417 1358 CTCCCCCGTCTGGCTTTGGCTCCCCTTCTTCTCTCTCTGCGCGCGCATGGCCTGTTCGAT 1417 361 GCTGTTCCCCAATTGATCTCCATGAGTGAGAGAGATAGCTGGATTAGGCGATCGCGCTTC 420 [B1 GTGTGGCGCGGCCGCGCGTCGGAGTGGCGCGCGCTCGGAGCGGAGCGGAGGGGCGG 2	61 TCTCCATCACTCGGGTTCCGCGCTGCATTTCGGCCGGCGGGTTGAGTCAGATCTGGGCGA 120	99.1%; Score 2127; DB 2; Length 11473; 7; Conservative 0; Mismatches 0; Indels 10; CGCCAGCTTCCACCCCGCCGCACACGTTGCTCCCCCTTCTCATCGCTTCTCA	rice or maize. The methods and products can be used for targeting expression specifically to the endosperm of the seeds of cereal plants such as wheat or barley. They can be used for the expression of e.g. antisense sequences of granule-bound synthase (GBSS), SBE II, low mol. wt. glutenin, grain softness protein I, bacterial isoamylase, bacterial glycogen synthase, and wheat high mol. wt. glutenin Bx1. They can be used for modifying the characteristics of starch produced by a plant. The present sequence represents the SBE II gene sequence. (Updated on 17-OCT-2003 to standardise OS field) Sequence 11473 BP; 3096 A; 2263 C; 2423 G; 3691 T; 0 U; 0 Other;
& B & B & B & B	\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	00 00 00 00 00 00 00 00 00 00 00 00 00	8 8 8 8	אם אם אם אם אם אם אם	S B S B S	25 55 55 55 55 55 55 55
2738 TGGATTGGAAGCATTTTCTCGTGGTTATGAAAGCTTGGATTTACCCGCAGGTAAATTTA 2797 1731 AAGCTTTATTATTATGAAACGCCTCCACTAGTCTAATTGCATATCTTATAAGAAATTTA 1790	551 GGCCTTTTTGTT 618 GGCCTTTTTGTT 611 TGGATTCAACAC 611 TGGATTCAACAC 678 TGGATTCAACAC 671 TGGATTGGAAGC	2438 TTGATGGCTACAATTTGCTAAAATGCAATACGAATAACTGTCTCCGATCATTACAATT 2497 1431 AAAGAGTGGCAAACTGATGAAAATGTGGTGGATGAGTATAAGATTTTACTTTGCTAATTC 1490	TTGAATTAAGGTCCTTTCATCATGCAAATTTGGGGAACATCAAAGAGACAAAGACTAAGG ACCACCATTTCATACAGATCCCTTCGTGGTCTGAGAATATGCTGGGAAGTAAATGACTATAA ACCACCATTTCATACAGATCCCTTCGTGGTCTGAGAATATGCTGGGAAGTAAATGTATAA ACCACCATTTCATACAGATCCCTTCGTGGTCTGAGAATATGCTGGGAAGTAAATTGTATAA ACCACCATTTCATACAGATCCCTTCGTGGTCTGAGAATAACTGTCTCCGGATCATTACAATT TTGATGGCTACAATTTGCTCAAAATTGCAATACGAATAACTGTCTCCGATCATTACAATT 14			

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61 TCTCCATCACTCGGGTTCCGCGCTGCATTTCGGCCGGGGGTTGAGTGAG	1058 CGCCAGCTTCCACCCCCGCCGCACACGTTGCTCCCCCTTCTCATCGCTTCTCAATTAATA 1117	CCGCACACGTTGCTCCCCCTTCTCATCGCTTCTCAA1	Query Match 98.9%; Score 2124; DB 5; Length 11475; Best Local Similarity 99.9%; Pred. No. 0; Matches 2146; Conservative 0; Mismatches 0; Indels 2; Gaps 2;	Sequence 11475 BP; 3093 A; 2259 C; 2423 G; 3689 T; 0 U; 11 Other;	nutritional content by modulating the starch blosymthetic pathway to vary levels of amylopectin and/or amylose produced in the plant	ecially BEIID. The BEIID nucleic acids may be used to genetically sform cereal plants such as wheat or barley and for altering their	schli, designated F2. A. tauschli is likely to be the ancesti me donor of wheat. Probes isolated from the present sequence to identify type II starch branching enzymes (SBBs) in whee	Example 1; Fig 2; 103pp; English. The present sequence encodes a wheat starch branching enzyme of Aegilops	Y Nucleic acids encoding wheat starch branching enzyme IIb, useful for IIb altering the amylose and amylopectin content of cereal plants, e.g. wheat III and barley.	 Ν	Morell M, Rahman S;	(CSIR) COMMONWEALTH SCI & IND RES ORG. (GOOD-) GOODMAN FIELDER LID. (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.	EB-2000;	21-FEB-2001; 2001WO-AU000175.	30-AUG-2001.	WO200162934-41	ch biosynthetic pathway; amylopectin; F2; amylose;	it; starch branching enzyme; BEIIb; SBE; trans	eotide sequence	AAH78338; 26-NOV-2001 (first entry)	AAH78338 standard; cDNA; 11475 BP.		2091 CAGCATTAGTAGGTGACTTCAACAATTGGAATCCAAATGCAGATACTATGACCAGAG 2147	2031 CTGAATACTGACCAGTTACTATAAATTTATGATCTGGCTTTTGCACCCTGTTACAGTCTG 2090	3038 CAATTATTGTTAATGGTCACTATTCACCAACTAGCTTACTGGACTTACAAATTAGCTTA 3097	1971 CARTTATTGTTAATGGTCACTATTCACCAACTAGCTTACTGGACTTACAAATTAGCTTA 2030	2978 GAGAATGGGCTCCCTGGAGCGCATGTTATGTTCTTTTAAGTTCCTTAACGAGACACCTTC 3037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATTATGAAACGCCTCCACTAGTCTAATTGCATATCTTATAAGAAAATTTATAAATTCCTG 1799
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                                                                                                                                 TAGGTGACTTCAACAATTGGAATCCAAATGCAGATACTATGACCAGAG
                                                                                                                                                                                                                                GTTAATGGTCACTATTCACCAACTAGCTTACTGGACTTACAAATTAGCTTACTGAATACT
                                                                                                                                                                                                                                                                   CT-CCTGGAGCGCATGTTATGTTCTTTTAAGTTCCTTAACGAGACACCTTCCAATTTATT
                                                                                                                                                                                                                                                                                       CTCCCTGGAGCGCATGTTATGTTCTTTTAAGTTCCTTAACGAGACACCTTCCAATTTATT
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                                                   standard;
                                                                                                                 TAGGTGACTTCAACAATTGGAATCCAAATGCAGATACTATGACCAGAG
                                                                                                                                                                   GACCAGTTACTATAAATTTATGATCTGGCTTTTGCACCCTGTTACAGTCTGCAGCATTAG
                                                                                                                                                                                           GACCAGTTACTATAAATTTATGATCTGGCTTTTGCACCCTGTTACAGTCTGCAGCATTAG
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                                                                                                                                                                                                                                                                                                                                                                                       TTTTCCCCTCTCTTTTTCCAGTGCTGAAGGTATCGTCTAATTGCATATCTTATAAGAAA 1859
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26-NOV-2001 AAH78337

(first entry)

RESULT 4
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AAH78351; AAH78351

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                                                                                                                                                                                                                                                            Query Match
Best Local
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starch
                                                                                                                                                                                                                                                                                                                                  The present sequence encodes wheat starch branching enzyme 9, designated BEIIa. The specification describes BEIIb. BEIIb is a type II starch branching enzyme (SBE). The BEIIb nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the
                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding wheat starch branching enzyme IIb, useful altering the amylose and amylopectin content of cereal plants, eand barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of wheat starch branching
                                                                                                                                                                                                                                                                                                  Sequence 2726 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 1; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morell M,
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biosynthetic pathway; amylopectin;
                                                                                                             CCAAAGGAGTTAAGGAACTAGTCGTGGGGGAGAAACCGCGAGTTGTCCCAAAACCAGGAG
                                                                                                                                                                                                                      AGATACCTGAAGATATCGAGGAGCAAACGGCGGAAGTGAACATGACAGGGGGGGACTGCAG 1037
                       ACCEGTAATEC
                                                               ATGGGCAGAAAATATACGAGATTGACCCAACACTGAAAAGATTTTCGGAAGCCATCTTGACT 1217
                                                                                                                                                AAAAACTTGAATCTTCAGAACCGACTCAAGGCATTGTGGAAACAATCACTGATGGTGTAA
                                                                                                                                                                        AGAAACTTCAATCTTCAGAACCGACTCAGGGCATTGTGGAAACAATCACTGATGGTGTAA
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                                                                                               CCAAAGGAGTTAAGGAACTAGTCGTGGGGGAGAAACCGCGAGTTGTCCCAAAACCAGGAG
 ACCGATACAGO
                                               ATGGGCÁGAAAATATÁCGÁGÁTTGACCCAÁCGCTGÁÁAGATTTTCGGAGCCATCTTGACT
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                                                                                                                                                                                                                                                                                                  726 A; 564 C;
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  450
                         1228
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No. 2.5e-55;
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in; amylose;
                                                                                                                                                                                                                                                                                                  735 T; 0
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.g. wheat
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Best Local Similarity
Matches 212; Conserv
                                 Wheat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH78351-54 represent intron 5 fragments from wheat. The specification describes a wheat starch branching enzyme, designated BRIIb. BBIIb is type II starch branching enzyme (SBE). The BEIID nucleic acids may be used to genetically transform cereal plants such as wheat or barley an for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 226 BP; 64 A; 49 C; 40 G; 73 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                           AAH78353 standard; DNA; 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    produced in the plant
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biosynthetic pathway; amylopecti
                              starch branching enzyme; BEIIb; SBE; transgenic plant; biosynthetic pathway; amylopectin; amylose; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.3%;
                                                                                                                  of intron 5
                                                                                                                                                                               entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 177.6; DB 5;
Pred. No. 1.1e-39;
O; Mismatches 14;
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amylopectin; amylose; ss.
                                                                                                                     fragment from B genome of wheat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. wheat and barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 4; 103pp; English.
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                                                                                                                                                            Wheat; starch branching enzyme; BEIIb; SBE; transgenion starch biosynthetic pathway; amylopectin; amylose; se
21-FEB-2001;
                                                                                                                                                                                                                          Nucleotide
                                                                                                                                                                                                                                                                  26-NOV-2001
                                                                                                                                                                                                                                                                                                           AAH78352;
                                                                                                                                                                                                                                                                                                                                                 AAH78352 standard; DNA; 228
                                                                               WO200162934-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1956 TAACGAGACACCTTCCAATTTATTGTTAATGGTCACTATTCACCAACTAGCTTACTGGAC
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GOODMAN FIELDER LTD.
GRP LIMAGRAIN PACIFIC PTY LTD.
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                                                                                                                                                                                                                          sequence of intron 5 fragment from A genome
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  2001WO-AU000175
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Pred. No. 6.7e-36;
0; Mismatches 8
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Best Local S
Matches 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH78351-54 represent intron 5 fragments from wheat. The specification describes a wheat starch branching enzyme, designated BSIIb. BEIIb is a type II starch branching enzyme (SBE). The BEIIb nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-570635/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 4; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                      Rice type IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
01-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV05639;
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                                                                                                                                             mat_peptide
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                                                                                                                                                                                                                                                                                                                                                           type IV
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GOODMAN FIELDER LTD.
GRP LIMAGRAIN PACIFIC PTY
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                                                                                                                                                                                                                                                                                                                                                                                                          starch branching enzyme cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                   starch
                                                                                         /product=
                                                                                                                                                  288.
                                                                                                                                                                 /*tag= a
129. .287
/*tag= b
                                                                                                                                                                                                                                         Location/Qualifiers
129. .2654
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                              branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to mRNA;
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                                                                                                "type_IV_starch_branching_enzyme"
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Pred. No. 1.8e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                              enzyme; amylopectin synthesis;
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Best Local S
Matches 167
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1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes the rice type IV starch branching enzyme, which has the ability to synthesise amylopectin. The quality of starch improved by the use of the protein. (Updated on 25-MAR-2003 to correct field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rice starch branching enzyme gene - quality starch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-133625/13.
P-PSDB; AAW41763.
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                                           Chang H,
Katagiri
                                                                                                                                                                                                                                                                                                                                  Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                        Plant; bacterial gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice gene, SEQ ID 4612
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                                                                                                                                                                                                   22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                              03-JAN-2003
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                                                                                                                                                     22-JUN-2001; 2001WO-IB001105
                                                                                                          (SYGN ) SYNGENTA PARTICIPATIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3015 BP; 796 A; 606 C; 819 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACACTGAAAGATTTTCGGAGCCATCTTGACTACCGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; DNA;
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                                           Chen W, F, Quan
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TOATSU
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                                                                                                                                                                                                                                                                                                                                                                                               infection; fungal infection; viral infection; rice;
                                             Ś
                                             Cooper :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.3%;
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Pred. No. 3.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                             Glazebrook J, Goff\SA, whitham S, Xie Z, \Zhu
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WPI; 2003-175290/17

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Best Local Similarity
Matches 167; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a method (MI) for identifying genes involved in plant resistance or response to pathogenic infection. MI comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
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22-JUN-2001;
26-SEP-2001;
20-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2655 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                          carbohydrate degradation; carbohydrate; plant grain; grain filling; tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet; wheat; rice; protein; oil; starch; fibre; moisture content; cereal g
                                                                                                                                                                                                                                                                                                                                                                                                   wheat; rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant
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                                                                                                                                                                                                                                                                                                                                                                            gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rice DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC08218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC08218
                                                                                                                          21-JUN-2002;
                                                                                                                                                                                        03-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biotechnology; carbohydrate synthesis; carbohydrate metabolism;
hydrate degradation; carbohydrate; plant grain; grain filling; c
                                                                                                                                                                                                                                                                                                               sativa
                                                                                                                                                                                                                                                                                                                                                                      ds; plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCECTAAT 1226
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   2001US-0300112P.
2001US-0325277P.
2001US-0342327P.
                                                                                                                             2002WO-IB002450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq ID523 related to grain filling.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82;
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Best Local Similarity
Matches 164; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention, in the area of plant biotechnology, relates to novel polynucleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a contact for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/publishedpct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New plant genes encoding polypeptides having an activity involved in associated with the synthesis, metabolism or degradation of carbohydin the plant grain useful in generating plants having improved
                                             Wheat;
starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                              Nucleotide
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                                                                                                                                                                                                                                                                    527
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                                             starch brancl
biosynthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                CCAAAGGAGTTAAGGAACTAGTCGTGGGGGAGAAACCGCGAGTTGTCCCAAAACCAGGAG
                                                                                                                                                                                         standard; cDNA; 2968
                                                                                                                                                                                                                                                                                                                               ATGGGCAGAAGATATACCAAATTGACCCAATGCTGGAAGGATTTCGGAACCATCTTGACT
                                                                                                                                                                                                                                                                                                                                                          ATGGGCAGAAAATATACGAGATTGACCCAACACTGAAAGATTTTCGGAGCCATCTTGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2304 BP; 610 A; 457 C; 620 G; 617 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                  ACCG 530
                                                                                              sequence of wheat starch branching enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.4%;
ilarity 67.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W, Briggs S,
Katagiri F,
                                                                                                                           (first entry)
                                                             branching
                                               pathway;
                                                            enzyme;
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Kreps J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 116; DB 9;
Pred. No. 1.2e-21;
0; Mismatches 80
                                               me; BEIIb; SBE; amylopectin; an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moughamer
Ricke D;
                                                                                                 (BEIIb)
                                                               plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carbohydrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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1217

526

1157

466

1097

406

1037

346

Triticum

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RESULT 11
ABK15494
ID ABK15494
ABK15494
ABC ABK15
XX
AC ABK15
XX
CORNAR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a wheat starch branching enzyme, designated BEIIb. BEIIb is a type II starch branching enzyme (SBE). The BEIIb nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Fig 9; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200162934-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morell M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2000; 2000AU-00005742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2001; 2001WO-AU000175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                        Wheat; starch branching enzyme; starch synthesis; wdk2c.pk009.j17; antibody; gene mapping; expresse
                                                                                                                                                                                                                                                                           08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CSIR )
                                                                                                                                                        gene;
                                                                                                                                                                                                                                     Wheat starch
                                                                                                                                                                                                                                                                                                                                                      ABK15494
                                                                                                                   Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-570635/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMONWEALTH SCI & IND RES ORG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOODMAN FIELDER LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTGTGGAAACAATCACTGATGGTGTAACCAAAGGAGTTAAGGAACTAGTCGTGGGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGTGAACATGACAGGGGGGACTGCAGAGAAACTTCAATCTTCAGAACCGACTCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2968 BP; 784 A; 626 C;
                                                                                                                                                                                                                                                                                                                                                    standard; cDNA; 3039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAATTACGCATTCTGCCACCACCGGGAAATGGACAGCAAATATACGAGATTGACCCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACCGCGAGTTGTCCCAAAAACCAGGAGATGGGCAGAAAATATACGAGATTGACCCAACA 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTGAAGAAATTGATGCTGAAGACACGAGCAGAATGGACAAAGAATCATCTACGAGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAACAAGCCTACAGGATGGAGGTGAAGATAGTATTTGGTCTTCAGAGACAAATCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCGAGACTTTAAGTACCATCTTGAGTATCGATATAGCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAAAGATTTTCGGAGCCATCTTGACTACCGGTAATGCCTA 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rahman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.9%;
ilarity 61.3%;
Conservative
                                                                                                                                                                                                                                   branching enzyme IIb cDNA
                                                                                                                                                                                                                                                                         (first entry)
/*tag= a
/product=
/partial
                                                                           location/Qualifiers
                        "Starch branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 84.4; DI
Pred. No. 1.2e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                        βP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; DB 5;
1.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   756 T;
                                                                                                                                                                                                                                         from
                                                                                                                                                                            expressed
                      enzyme IIb"
                                                                                                                                                                                                                                     clone wdk2c_pk009.j17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٦;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                transgenic plant;
d sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 Other;
                                                                                                                                                                              sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     676
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멍 Ş 뭐 Ş 뮍 8

1070

1129 431

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491

551

432

S

CTGAAAGATTTTCGGAGCCATCTTGACTACCGGTAATGCCTA

AAATTACGCATTCTGCCACCACCGGGAAATGGACAGCAAATATACGAGATTGACCCAACG дадссеседеттетсссаладссаваратеевсавалататасваваттвасссавса 1189 AGTGAAGAATTGATGCTGAAGACACGAGCAGAATGGACAAAGAATCATCTACGAGGGAG GAAACAAGCCTACAGGATGGAGGTGAAGATAGTATTTGGTCTTCAGAGACAAATCAGGTT

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This invention relates to the cDNA and protein sequences of a novel wheat companies to the cDNA and protein sequences of a novel wheat starch branching enzyme IIb enzyme. Starch branching enzymes are consisted for the formation of alpha 1-6 linkages in amylopectin in the constitution synthesis pathway. The nucleotide sequence in amylopectin in the constitution is the constitution of the protein in the constitution of the invention is constitution of the protein in situation in the constitution of the protein in situation cells, or in vitro in cell extracts. The protein is constituted in the constitution of expression of a starch branching enzyme IIb protein in cell extracts. The protein is constitution of expression of a starch branching enzyme IIb protein or enzyme constitution is useful as markers for traits linked to those genes. This constitution is useful in plant breeding in order to develop lines with considering the constant of the protein of the nucleotide connectives. A polynucleotide fragment is useful for isolating connection. Constitution from the constitution protein is safety are also useful as DNA hybridisation probes or as constitution fragment length polynorphism markers. Nucleic acid probes constitution fragment length polynorphism markers. Nucleic acid probes constitution processence in situ hybridisation (FISH) mapping. The present constitution constitu
                                                                                                        Query Match
Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated polypeptide having starch IIb enzyme activity, use: preparing antibodies to the proteins which are used to detect the polypeptides in situ in cells or in vitro in cell extracts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2000; 2000US-0186098P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-FEB-2001; 2001US-00792127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2002002713-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 17-18; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ALLE/)
(BECK/)
                                                                                                                                                                                                                                                                    Sequence 3039 BP; 836 A; 624 C; 783 G; 796 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PEAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-178959/23.
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BECKLES D M.
BUTLER K H.
PEARLSTEIN R
GAAGTGAACATGACAGGGGGGGACTGCAGAGAAACCTTCAATCTTCAGAACCGACTCAGGGC 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beckles DM,
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "No start codon shown. The sequence from nucleotides 481-3039 is specifically claimed in of the specification and is shown as Seq ID. 1
                                                                                                                                                   3.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Butler KH,
                                                                                                                0
                                                                                                                Score 84.4; DB 6;
Pred. No. 1.3e-12;
0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pearlstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₩;
                                                                                                                                                                                              Length 3039;
                                                                                                                         Indels
                                                                                                                     °.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     claim
                                                                                                                         Gaps
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552

CTCCGAGACTTTAAGTACCATCTTGAGTATCGATATAGCCTA 593

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RESULT 12
AAH78341
ID AAH78
XX AAH78
XX 26-NC
CT 26-NC
CXX Wheat
KW Wheat
KW Starc
XX Aegil
XX IIIII
XX Aegil
XX The I
CC Star
CC Is IIII
CC Star
CC Is IIIII
CC Star
CC Is IIII
CC STAR
CC IS IIIII
CC STAR
CC IS IIII
CC STAR
CC IS IIII
CC STAR

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Best Local S
Matches 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a partial genomic sequence of a wheat starch branching enzyme of Aegilops tauschi, designated F2. A. tauschii is likely to be the ancestral D genome donor of wheat. Probes isolated F2 were used to identify type II starch branching enzymes (SBEs) in wheat, especially BEIIb. The BEIIb nucleic acids may be used to genetically transform cereal plants such as weit or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. {\bf v}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH78341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2001; 2001WO-AU000175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200162934-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aegilops tauschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wheat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Partial sequence of a starch branching enzyme designated F2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3962 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CSIR )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 132; Conserv
1336
                                                                                                                                                                                                                                  1216
                                                                                                                                                                                                                                                                                                                                                                                                                   1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      starch branching enzyme; BEIIb; SBE; transgenic plant; biosynthetic pathway; amylopectin; F2; amylose; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMONWEALTH SCI & IND RES
GOODMAN FIELDER LTD.
GRP LIMAGRAIN PACIFIC PTY I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                    APACCGCGAGTTGTCCCAAAACCAGGAGATGGGCAGAAAATATATACGAGATTGACCCAACA 1189
                                                                                                                                                                                                                                                                                                                                                           GAAACAAGCCTACAGGATGGAGGTGAAGATAGTATTTGGTCTTCAGAGACAAATCAGGTT 1215
                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGTGAACATGACAGGGGGGACTGCAGAGAAACTTCAATCTTCAGAACCGACTCAGGGC
                                                       CTGAAAGATTTTCGGAGCCATCTTGACTACCGGTA 1224
                                                                                                                                                                                                                                     AGTGAAGAATTGATGCTGAAGACACGAGCAGAATGGACAAAGAATCATCTACGAGGGAG
                                                                                                                                                                                                                                                                                          <u> АТТСТССАЛАСЛАТСАСТСАТССТВАССЛААССАСТТВАССАСТАСТССТСССССАС</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.8%;
nilarity 61.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rahman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000AU-00005742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; 103pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1091 A; 778 C; 809 G; 1284 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PACIFIC PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 82.2; DB 5;
Pred. No. 6.2e-12;
0; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3962;
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                                                                                                                                                                                                                                                                                                1129
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RESULT

13

RESULT 14
AAQ73750
ID AAQ73
XX
AC AAQ73
XX

standard; cDNA to mRNA;

2919 å

AAQ73750, AAQ73750 멂 Ş 밁 Ś 片 Ś

뮍 5

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AAH78343
IID AAH7
XX AAH7
AC AAH7
XX Part
PP PO NO2(
XX Part
PP PO NO2(
PP N
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a partial genomic sequence of a wheat starch branching enzyme, designated BEJID. BEJID is a type II starch branching enzyme (SBE). The BEJID nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH78343 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding wheat starch branching enzyme IIb, useful altering the amylose and amylopectin content of cereal plants, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     starch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Partial genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 95-98; 103pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-570635/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morell M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200162934-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8381 BP; 2134 A; 1788 C; 1829 G;
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1190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMONWEALTH SCI & IND GOODMAN FIELDER LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRP LIMAGRAIN PACIFIC PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                       GAAACAAGCCTACAGGATGGAGGTGAAGATAGTATTTGGTCTTCAGAGACAAATCAGGTT
                                                                                                                                                                                                                                                                                                                                         AAACCGCGAGTTGTCCCAAAAACCAGGAGATGGGCAGAAAATATACGAGATTGACCCAACA
  CTGAAAGATTTTCGGAGCCATCTTGACTACCGGTA
                                                     AAATTACGCATTCTGCCACCACCGGGAAATGGACAGCAAATATACGAGATTGACCCAACG
                                                                                                                                                                         AGTGAAGAATTGATGCTGAAGACACGAGCAGATGGACAAAGAATCATCTACGAGGGAG
                                                                                                                                                                                                                              ATTGTGGAAACAATCACTGATGGTGTAACCAAAGGAGTTAAGGAACTAGTCGTGGGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rahman
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 9.5e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8381;
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                                                                                                                                                                                  1735
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Starch Rice starch 05-JUL-1995

branching enzyme; rice; starch content;

branching enzyme (first entry)

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RESULT 15
ADC07807
ID ADC07
XX
AC ADC07
XX
AC ADC07
XX
DT 18-DE
XX
DE Rice
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Best Local S
Matches 122
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5'UTR
                                                                                                                                                                                                                                                                                                                                             The rice starch branching enzyme is encoded by the cDNA sequence AAQ73750. The starch content of rice grains can be increased by increasing the expression of branching enzyme in rice plants
                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 9-12; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                           New gene of branching enzyme of rice starch - useful for increasing starch yield of grain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP06261767-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
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 Rice DNA sequence Seq ID73
                      18-DEC-2003
                                                              ADC07807
                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                            1159
                                                                                                                                     1219
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DB; AAR60811.
                                                                                                                                                        556
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                                                                                                                                                                                                                                                                                  al Similarity 63.1
122; Conservative
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                                                                                                                                                                                                                                                              GAAACTTCAATCTTCAGAACCGACTCAGGGCATTGTGGAAACAATCACTGATGGTGTAAC 1098
                                                                                                                                     CCGGTAATGCCTA 1231
                                                                                                                                                                                                   GAGAGTGGTTGAAGAATTAGCTGCTGAGCAGAAACCACGAGTTGTCCCACCAACAGGAGA
                                                                                                                                                                                                                  CAAAGGAGTTAAGGAACTAGTCGTGGGGGGAGAAACCGCGAGTTGTCCCAAAAACCAGGAGA
                                                                                                                                                                                                                                          GGAGGTTGGAGCTGAAGTTGAGATTGAGTCATCTGGAGCAAGTGACGTTGAAGGCGTGAA 495
                                                                                                                                                                                                                                                                                                                             2919 BP; 755 A; 590 C; 800 G; 774 T; 0 U; 0 Other;
                                                             standard; DNA; 2307
                                                                                                                                                                             TGGGCAGAAAATATACGAGATTGACCCAACACTGAAAGATTTTCGGAGCCATCTTGACTA
                                                                                                                 TCGATATAGCCTA 628
                                                                                                                                                         TGGGCAAAAATATTCCAGATGGACTCTATGCTTAATGGCTATAAGTACCATCTTGAATA
                     (first entry)
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128. .322
/*tag= b
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/product= "branching_enzyme"
2603 . .2919
/*tag= d
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                                                                                                                                                                                                                                                                                            3.7%;
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  related
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Pred. No. 3.2e
0; Mismatches
  ö
  grain filling
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Matches 95
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                                                                                                                                                                                                      This invention, in the area of plant biotechnology, relates to novel polymicleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, cannola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence encoding a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format directly from WIPO at the publishedpot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved nutritional properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUN-2001; 2001US-0300112P.
26-SEP-2001; 2001US-0325277P.
20-DEC-2001; 2001US-0342327P.
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                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUN-2002; 2002WO-IB002450
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       1677
                                      364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; SEQ ID NO 73; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheng W, Briggs S,
ook J, Katagiri F,
                                                                                                                        Similarity
                                                              AACAGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGA-CCAACATGAAGGTGGATT 1676
   GGAAGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
                                                                                                                                                                          2307 BP; 608 A; 465
                                      ACCGGATACAGTGAATACAAGAGAATGCGTGCAGCTATTGACCCAACATGAAGGTGGCTT
                                                                                                          Conservative
                                                                                                                        3.7%;
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Kreps J,
                                                                                                          Score 78.6; Di
Pred. No. 4.7e
O; Mismatches
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, Provart N,
                                                                                                                    6; DB 9;
4.7e-11;
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                                                                                                                                          Length 2307;
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Ricke D;
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Search completed: April 10, 2004, 04:00:00 Job time : 846.046 secs

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424

GGATGCATTTTCTCGTGGTTACGAAAAGCTTGGATTCACCCGCAG

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Result
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Maximum DB
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 summaries
 Issued_Patents_NA:*
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/cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptcdata/2/ina/backfiles1.seq:*
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US-09-257-894-9
US-09-257-894-1
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US-09-257-894-5
US-09-257-894-5
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US-09-251-976-2813
US-09-252-991A-8298
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US-09-252-991A-8018
US-09-252-991A-8018
US-09-253-991A-8018
US-09-253-991A-8018
US-09-303-333D-184
US-09-105-537-3
US-09-105-537-3
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Patent No. 5196304
Sequence 184, App
Sequence 19, Appl
Sequence 3, Appli
Sequence 19, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 19, Appli
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                                                      3, Appli
14, Appl
11, Appl
9, Appli
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                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
LENGTH: 2853
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                               Best
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                                       1218
                                                                          1158
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                       ACCGATACCGC
                                      ACCGGTAATGC 1228
                       522
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330 44552 2830 1664976 44103765 44103765 112729 112729 112732 12560 44103 12732 3	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.8	36.8	37.2	37.2	37.2	37.2	37.6	37.6	37.6	37.6	37.6
44425125 4444443344331	1.7	1.7	1.7	1.7	1.7	1.7	1.7		1.7	1.7	1.7	1.7	1.7	1.8	1.8	1.8	1.8	1.8
4 US-09-313-294A-7001 4 US-09-434-288-10 2 US-09-434-288-10 2 US-08-475-844-4 5 PCT-US95-08429-4 1 US-07-882-292-1 2 US-08-31-444-1 5 PCT-US93-04-102-1 4 US-08-916-421B-1 3 US-09-103-840A-2 3 US-09-103-840A-1 4 US-09-252-991A-16329 4 US-09-252-991A-16329 4 US-09-252-991A-16329 4 US-09-252-991A-16329 4 US-09-252-991A-16555 4 US-09-894-844-47 5 US-09-894-844-47 6 US-09-616-2891A-16555 8 US-09-616-2891A-18555 9 US-09-616-2891A-18555	12732	2561	1980	1296	1272	1029	441	4411529	4403765	1664976	2830	2830	2830	4252	4252	1600	395	330
US-09-1313-294A-7091 US-09-434-288-10 US-08-475-444-4 US-08-475-444-1 US-07-882-292-1 US-08-331-444-1 PCT-US93-04102-1 US-08-916-421B-1 US-09-103-840A-2 US-09-103-840A-1 US-09-252-991A-16157 US-09-252-991A-16157 US-09-252-991A-16555 US-09-894-844-47 US-09-252-991A-16555 US-09-894-844-47 US-09-103-894-88 US-09-616-756-1	w	4.	4	4	4	4.	4	W	ω	4,	ហ	N	Н	IJ	N	4	4	4
	US-09-060-756-1	US-09-616-289-48	US-09-252-991A-16555	US-09-894-844-47	US-09-252-991A-16045	US-09-252-991A-16157	US-09-252-991A-16329	US-09-103-840A-1	US-09-103-840A-2	US-08-916-421B-1	PCT-US93-04102-1	US-08-331-644-1	US-07-882-292-1	PCT-US95-08429-4	US-08-475-844-4	US-09-434-288-10	US-09-894-844-45	US-U9-313-294A-7061

ALIGNMENTS

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Sequence 3, Application US/09609040

Patent No. 6570066

GENERAL INFORMATION:
APPLICANT: Willmitzer, et al.
TITLE OF INVENTION: WUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRAT!
TITLE OF INVENTION: CONCENTRATION AND COMPOSITION IN PLANTS
FILE REFERENCE: 514413-3515.1

CURRENT APPLICATION UNMBER: US/09/609,040

CURRENT APPLICATION NUMBER: DCT/EP92/00302

PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 1992-02-11

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: CDS
LOCATION: (313)..(2499)
OTHER INFORMATION: BRANCHING ENZYME
                                                                                                                                                                                                                                                                                                                                                                             h 11.3%;
Similarity 98.0%;
46; Conservative
                                                                                                                                                                                                                          AGAAACTTCAATCTTCAGAACCGACTCAGGGCATTGTGGAAACAATCACTGATGGTGTAA
                                                                                                                                                                                                                                                                                                           AGATACCTGAAGATATCGAGGAGCAAACGGCGGAAGTGAACATGACAGGGGGGGACTGCAG
                                                                                                                                 CCAAAGGAGTTAAGGAACTAGTCGTGGGGGGAGAAACCGCGAGTTGTCCCCAAAACCAGGAG
                                                                                                                                                                                                                                                                                  AGATACCTGAAGATATCCAGGAGCAAACGGCGGAAGTGAACATGACAGGGGGGGACTGCAG
                               ATGGGCAGAAAATATACGAGATTGACCCAACACTGAAAGATTTTCGGAGCCATCTTGACT
                                                                                                                                                                                       AAAAACTTCAATCTTCAGAACCGACTCAGGGCATTGTGGAAACAATCACTGATGGTGTAA
ATGGGCAGAAATATACGAGATTGACCCAACACTGAAAGATTTTCGGAGCCATCTTGACT
                                                                                          CCAAAGGAGTTAAGGAACTAGTCGTGGGGGAGAAACCGCGAGTTGTCCCAAAACCAGGAG
                                                                                                                                                                                                                                                                                                                                                                          Score 243; DB 4; I
Pred. No. 1.8e-60;
0; Mismatches 5;
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US-09-731-166-9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified
FILE REFERENCE: 35718/206348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/731,166
CURRENT APPLICATION NUMBER: US/09/731,166
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09731166
Patent No. 6639126
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: SBEIIA
OTHER INFORMATION: Genbank Accession No. 6639126 U65948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                             APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OCATION: (2)...(2446)
                                                                                                                        COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                        STREET: 1800 Dia
CITY: Alexandria
                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1067 GGCATTGTGGAAACAATCACTGATGGTGTAACCAAAGGAAGTTAAGGAACTAGTCGTGGGG 1126
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      US/07/935,313
                                                                                     US/08/232,463
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                                                                                                                              Version
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SOFTWARE: Fast SEQ ID NO 11 LENGTH: 2720

FastSEQ for Windows Version

TYPE: DNA

ORGANISM: Zea mays

PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-1 NUMBER OF SEQ ID NOS:

1999-12-06

CURRENT APPLICATION NUMBER: US/09/731,166

2000-12-06 3ER: 60/169,993

GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified
FILE REFERENCE: 35718/206348

Polysaccarides

Sequence 11, Application US/09731166 Patent No. 6639126

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RESULT 4
US-09-731-166-11
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                           1092
                                                                  579 CTATTGTAGTCATCCTTGCATTTTGCAGGCGCCGTCCTGAGCCG
                                                                                                              519 TATTITCTCATTCTTTCTTCCTGTTCTTGCTGTAACTGCAAGTTGTGGCGTTTTTTCA 578
                                                                                                                                                                                                                                                                                                                                                  219
                                                                                                                                      GTGTCACCCAGGCCCTGGTGTTACCACGGCTTTGATCATTCCTCGTTTCATTCTGATATA 518
                                                                                                                                                                                                                                 BENT,
                                                                                         CTGGATTAGGCGATCGCGCTTCCTGAACCTGTATTTTTTCCCCCGCGGGGAAATGCGTTA 458
                                                                                                                                                                                                                                                                                                                                                                                                                               pTZgpt-F1s
                                                                                                                                                                                                                                                                                                                                                                       3.2%; Score 68.8; DB 1; ilarity 4.7%; Pred. No. 2.7e-09; Conservative 234; Mismatches 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
APPLICANT: Lightner, Jonathan E.
APPLICANT: LIGHTNER, No. 5376749el
TITLE OF INVENTION: Expression of
TITLE OF INVENTION: Enzyme Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Query Match
Best Local Similarity
Matches 74; Conserv
                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
APPLICATION NUMBER: 0, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,73
REFERENCE, DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
                                                                                                                                                                  TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2087 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (0)...(0)
OTHER INFORMATION: SBEILD
OTHER INFORMATION: Genbank Accession No.
NAME/KEY: CDS
LOCATION: (101)...(2500)
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
                                                                        STRANDEDESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
1-257-894-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 2.9%;
Local Similarity 76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/257,894 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Wilmington
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                                                                                                                           nucleic acid
DEDNESS: single
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 2.7%;
ilarity 74.0%;
Conservative
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Expression of Starch Biosynthesis
Enzyme Genes
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Pred. No. 1.9e-07;
0; Mismatches 24
   Score 58.4; DF Pred. No. 1.4e-0; Mismatches
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                 ; DB 4;
1.4e-06;
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                                       Length 2087;
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US-09-257-894-8/c
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; MOLECULE TYPE:
US-09-257-894-8
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Patent No. 6376749
                                                                                                                                      Matches
                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                             TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09,
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/09:
APPLICATION NUMBER: 10, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Broglie,
APPLICANT: Klein, Th
APPLICANT: Hubbard,
APPLICANT: Lightner,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: POSTEM: Microsoft Windows
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            NAME: Majarian, William R.
REGISTRATION NUWBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                  1675 GGTACAGCCTCTATAGAAGAATCCGTTCAGACATTGATGAACATGAAGGAGGCTT
                                                                                                  1622 GATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATTGGAAG
                                  1682 CATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
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CCTTCTCCCGTAGTTATGAGAAGTTTGGATTTAATGCCAG, 1576
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Hubbard, Natalie L.
                                                                                                                                      Conservative
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No. 6376749el Starches via Modification
Expression of Starch Biosynthesis
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                                                                                                                                      Score 58.4; DB 4;
Pred. No. 1.4e-06;
0; Mismatches 26;
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                                                                                                                                                                        Length 2165;
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RESULT 7 US-09-257-894-1

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LOCATION:
US-09-257-894-1
                                                               Sequence 14, Application US/08941445A
Patent No. 6107060
GENERAL INFORMATION:
APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanping
                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: Lightner,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICATION NUMBER: 09/0
FILING DATE: JUNE 10, 19
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB
TELECOMMUNICATION INFORMATION:
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APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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TOPOLOGY: linear
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o. 6376749
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                                                                                                                                                                                                                              CCTTCTCCCGTAGTTATGAGAAGTTTGGATTTAATGCCAG 590
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Lightner, Jonathan
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79..2476
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Pred. No. 1.6e-06;
0; Mismatches 26;
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; Sequence 1, Application US/09087277B
patent No. 616926
; RENERAL INFORMATION:
APPLICANT: EK, Bo
APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II
FILE REFERENCE: 003300-486

CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558

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RESULT 9
US-09-087-277-1
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APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (303) 499-80 INFORMATION FOR SEQ ID NO:
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NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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NAME/KEY:
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LENGTH: 2725 base pair
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
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91..264
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265..2487
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Pred. No. 1.6e.
0; Mismatches
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; EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver: 2.0
; SEQ ID NO 1
; SEQ ID NO 1
                                                                  RESULT 10
US-09-658-499-1
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                                                                                                                                                                                                                                                                                         ; FEATURE:
; NAME/KBY: misc_feature
; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid
US-09-087-277-1
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GENERAL INFORMATION:
APPLICANT: EK, Bo
APPLICANT: KHOSNOODI,
                                      Sequence 1, Application Patent No. 6469231
                                                                                                                                                                                                                                     Matches
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FEATURE: sig_peptide LOCATION: (189)...(332)
FEATURE:
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NAME/KEY: misc feature
LOCATION: (92)...(2156)
OTHER INFORMATION: Nucleotides
OTHER INFORMATION: n wherein n
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LOCATION: (189)..(2825)
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OTHER INFORMATION:
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NAME/KEY: misc feature
LOCATION: (1896)..(1898)
OTHER INFORMATION: Amino acid
OTHER INFORMATION: or Phe.
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LOCATION: (1404)..(1406)
OTHER INFORMATION: Amino
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION: Amino
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LOCATION: (285)..(287)
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LOCATION: (333)..(2825)
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Pred. No. 2
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TITLE OF INVENTION: STARCH BRANCHING ENZYME II
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/658,499
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 09/087,277
PRIOR FILING DATE: 1998-05-29
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: PCT/SE96/01558
PRIOR APPLICATION NUMBER: SE 9504272-7
PRIOR PILING DATE: 1995-11-29
PRIOR PILING DATE: 1995-11-29
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LOCATION: (189)..(2825)
NAME/KEY: sig_peptide
LOCATION: (189)..(332)
NAME/KEY: mat_peptide
LOCATION: (333)..(2825)
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SOFTWARE: PatentIn Ver.
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PRIOR FILING DATE: 1996-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Nucleotides 92, OTHER INFORMATION: n wherein n = A, NAME/KEY: misc feature LOCATION: (285)...(287) OTHER INFORMATION: Amino acid -16 j OTHER INFORMATION: or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Unknown Organism:beII gene OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum OTHER INFORMATION: (potato)
                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (1896)...(1898)
OTHER INFORMATION: Amino a
OTHER INFORMATION: or Phe-
                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino
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LOCATION: (1404)..(1406)
OTHER INFORMATION: Amino
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LOCATION: (92)..(2156)
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ORGANISM: Unknown
FEATURE:
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LOCATION: (2154)..(2156)
OTHER INFORMATION: Amino
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                             1679 AAGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
835
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AAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAG
                                                               ACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTT
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Pred. No. 2e-0
0; Mismatches
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RESULT 11
US-09-257-894-5/c
US-09-257-894-5/c
; Sequence 5, Application U
; Sequence 10, 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, X

US/09257894

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                                                                                                                                                                                                                               equence 14, Application US/08232463 atent No. 5670367
                                                                                                                                                                                                                                                                     08-232-463-14/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US
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                                                                                                                                                                 APPLICANT: SCHEIFLINGER, APPLICANT: FALKNER, F. G.
                                                                                                              CORRESPONDENCE
                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM FC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: JUNE 10, 1998
TORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
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APPLICATION NUMBER: 0
FILING DATE: JUNE 10,
COUNTRY: USA
ZIP: 22313-0299
MPUTER READABLE
                                                                                 STREET:
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                                                                 ITY: Alexandria
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                                                                                 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 302-992-4926
302-773-0164
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                                                                                                Foley & Lardner
                                                                                                                  ADDRESS
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   FORM:
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Pred. No. 1
                                                                                   Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Best Local 9
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                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                   CLONE:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                              ELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                              1382
                       1147 AAAACCAGGAGATGGGCAGAAAATATACGAGATTGACCCAACACTGAAAGA 1197
                                                                                                                                                                     Similarity 2.6%; Pre 6; Conservative 145;
                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                     GGGGACTGCAGAGAAACTTCAATCTTCAGAACCGACTCAGGGCATTGTGGAAACAATCAC 1086
                                                                              TGATGGTGTAACCAAAGGAGTTAAGGAACTAGTCGTGGGGGAGAAACCGCGAGTTGTCCC 1146
                                                                                                                                                                                               TTTCGTGCTGTAGATACCTGAAGATATCGAGGAGCAAACGGCGGAAGTGAACATGACAGG 1026
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                                                                                                                                                                                                                                                                                                                                                                      7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                 (703)683-4109
                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                               (703)836-9300
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                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                         2.1%; Scor
2.6%; Pred.
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                                                                                                                                                                                                                                          Score 45; DB 1; red. No. 0.024;
                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                               80;
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US-09-621-976-2813

/ Sequence 2813, Application US/09621976

/ Sequence 2813, Application US/09621976

/ Sequence 2813, Application US/09621976

/ Sequence 1 NFORMATION:

/ APPLICANT: Dumas Milne Edwards, J.B.

/ APPLICANT: Dumas Milne Edwards, J.B.

/ APPLICANT: Obert, S.

/ APPLICANT: Glordano, J.Y.

/ TITLE OF INVENTION: ESTS and Encoded Human Proteins.

/ FILE REFERENCE: GENSET.054PR2

/ CURRENT APPLICATION NUMBER: US/99/621,976

/ CURRENT FILING DATE: 2000-07-21

/ NUMBER OF SEQ ID NOS: 19335

/ SOFTWARE: Patent.pm

/ SEQ ID NO 2813

/ LENGTH: 832

/ TYPE: DIA

ORGANISM: Homo sapiens

/ FEATURE:

NAME/KEY: CDS

LOCATION: 235.399
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US-09-621-976-2813

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APPLICANT: It, Laura Y.

APPLICANT: It, Laura Y.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYMUCLEOTIDES AND POLY

FILE REFERENCE: PL-0017 US

CURRENT APPLICATION NUMBER: US/09/313,294A

CURRENT FILING DATE: 199-05-14

NUMBER OF SEQ ID NOS: 7600

SOFTWARE: PERL Program

SEQ ID NO 3795

LENGTH: 279

TYPE: PN"
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FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyt
NAME/KEY: unsure
LOCATION: 125-126
OTHER INFORMATION: a, t,
US-09-313-294A-3795
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US-09-313-294A-3795
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Patent No. 6476212
GENERAL INFORMATION:
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                                195
                                                                                     135 CACTACGCGGGGATGGCGACGTTCGCGGTGTCCGGGGGCCC 194
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94
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                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RCWK-----KKAYYRKTTCYSSKGWTWWKRWKKAWTTWWWKKTYYWAATRYWWMCWTKR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RWYWWKYTTWYAKCWTKWKWSWSYWMYWKWYYMKTYWRWRRKKKKAWWKYWKTWTWWYWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WWAWR 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GÅGMKAWRASCMMRRKYAGKSKTSYKSMWMCWTRSWKYCYTKARWTGYYCYRKGGMWGKR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WRASWWYCWWWGKARKWSTWRKSRSYASARSAKRCCYSCSWGAMSWKYMWRMWRWRGWAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRWYASKKYMWKRWWWCWARMYRYSTGTRASMWWRRWYYIMMMKWWKYAWARAAWRWWAM 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAGCTTACTGAATACTGACCAGTTACTATAAATTTATGATCTGGCTTTTGCACC-CTGTT 2082
                                CCCTAATCGGCGATGGCGACGGTGGCGATGGACATCTCGAAGCCCCACTCCAGTGGCGTCC
GGCGACGAGGCCGCGGCGGCGAAGGGGANNAGCGGCGGAGGGGGCGAGGGGCTGCGG
                                                                                                                                     Conservative
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                                                                                                                                    Score 42.2; DB 4; Length 279; Pred. No. 0.021; O; Mismatches 50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17202, Appatent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 1.9%; Score 41.2; DB 4; Length 364;
Local Similarity 11.2%; Pred. No. 0.049;
hes 31; Conservative 131; Mismatches 114; Indels
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                                                                                  WYMRASMKKSKYCAWSRKGSKCCMYSRKGSKSCYCC
                                                                                                                                                                                                                                                                                                                                 ASCKYKGGKMACMTCWSTGAMYRYMASYGWCYSYMARYYTCYSKYRMWKYCYRKYRSRGM 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCGGCGGGTTGAGTGAGATCTGGGCGACTGACTCAATCACTACGCGGGGATGGCG
                                                                                                                           TCCTCTGCGCGCGCATGGCCTGTTCGATGCTGTTCC 368
                                                                                                                                                                   GMMSSMYGASKRMSSMCSASTRMSSÅSCMMYMMMSAGSYASCAWKMSKYRRCAKWSCTYS
                                                                                                                                                                                                         TCCTCTCGTACGCCTCGCTCTCTCGAATCTCCCCCGTCTGGCTTTGGCTCCCCTTCTCTC
                                                                                                                                                                                                                                                  CCMWCAGSGMCYSRSAGSRYSKKGSRGRWYWKKGCSRATSKKGRMMWMKKGSRRRATSRY
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                       2004, 14:13:07
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications NA:*

1: /cgn2 6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

2: /cgn2 6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2 6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

4: /cgn2 6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

4: /cgn2 6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

6: /cgn2 6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

7: /cgn2 6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

8: /cgn2 6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

9: /cgn2 6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

10: /cgn2 6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

11: /cgn2 6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

13: /cgn2 6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

14: /cgn2 6/ptodata/1/pubpna/USO0B_PUBCOMB.seq:*

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16: /cgn2 6/ptodata/1/pubpna/USO0B_PUBCOMB.seq:*

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Match Length DB
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10621.793 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd
12 US-10-434-893A-3

12 US-10-434-893A-1

12 US-10-434-893A-2

9 US-09-792-127-3

9 US-09-792-127-1

12 US-10-424-893A-4

9 US-09-792-127-1

12 US-10-424-599-130848

US-09-938-842A-337

11 US-09-938-842A-337

14 US-10-056-4454A-18

15 US-10-424-599-130849

15 US-10-397-954A-1

14 US-10-397-954A-1

15 US-10-397-954A-1

14 US-10-56-454A-17
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Sequence 3, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 130848,
Sequence 337, App
Sequence 37, Appl
Sequence 18, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10434893A

| Sequence 3, Application US/10434893A|
| Publication No. US20040060083A1|
| GENERAL INFORMATION:
| Applicant: Ahmed Regina |
| Applicant: Ahmed Regina |
| Applicant: Matthew Kennedy Morell |
| Applicant: Sadequr Rahman |
| TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and starch interest of INVENTION containing products with an increased amylose content |
| FILE REFERENCE: 69425 |
| CURRENT APPLICATION NUMBER: US/10/434,893A |
| CURRENT FILING DATE: 2003-05-09 |
| NUMBER OF SEQ ID NOS: 11 |
| SOCITWARE: PATENTIN Version 2.1 |
| SEQ ID NO 3 |
| LENGTH: 11476 |
| TYPE: DNA ORGANISM: Aegilops tauschii |
| FEATURE: NAME/KEY: MISC_FEATURE |
| LOCATION: (1):..(11476) |
| COTHER INFORMATION: n is a, c, g or t |
| FEATURE |
| COTHER INFORMATION: n is a, c, g or t |
| COTHER INFORMATION: n is a, c, g or t |
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US-10-434-893A-3
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2147; Conservative 0; Mismatches
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14 US-10-146-731-10
15 US-10-141-755-10
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1140 TTGTCC 2198 TTGTCC	1080 CAATCA 2138 CAATCA	1020 TGACA 2078 TGACA	960 TGCTAT	900 TCTAGC 1958 TCTAGC	840 TTGTTAG 1898 TTGTTAG	780 TGCGT0	720 CGGTA 1778 CGGTA	661 AGAG-0 1718 AGAGNO	601 TTGCA(1658 TTGCA(541 CTGTTV 1598 CTGTTV	481 ACCACG 1538 ACCACG	421 CTGAAC 1478 CTGAAC	361 GCTGTT 1418 GCTGTT	301 CTCCCC	241 ACTTGC 1298 ACTTGC	181 GTGTGG 1238 GTGTGG	121 CTGGCT 1178 CTGGCT	
CAAAACCAGGAGATGGG	CTGATGGTGTAACCAAAGGA 	AGGGGGACTGCAGAGAAACTTC 	TTTTCGTGCTGTAGATAC TTTTCGTGCTGTAGATAC	AAGAACTTCACAACATAATG(GCCTTGGCCCCGTGCTGGCTCTTGGGCCA 	TGCGTCAGGTTTCGAGCTTCTTCTATCA 	CGGTAAATCTTCATACAATCGTTATTCACTTA 	agag-gacgactiggcaagtcoggcgcaacctgaagaattacaggtacacacactc 	CAGGCGCCGTCCTGAGCCGCGCGGCGTCTCCAGGGAAGGTCCTGGTGCCTGAC	CTTGCTGTAACTGCAAGTTG 	GCTTTGATCATTCCTC GCTTTGATCATTCCTC	CTGTATTTTTTCCC CTGTATTTTTTCCC	CCCCAATTGAT CCCCAATTGAT	CGTCTGGCTTTGGCTCCCC	CGTCGCTGCTCCTCAGGAAG	CGCGGGCCGGCGTCGGAGTG	GACTCAATCACT GACTCAATCACT	
Cagaaaatatacgagattgac 	agttaaggaactagtcgtgg 	CAATCTTCAGA	CTGAAGATATCGACGAGCAAACGGCGGAAG 	CACCGTTTGGGGTTTCG	TCTTGGGCCACTGAAAAAATCAGAI	TCAGCATTGTGCAGTACTG	TCACTTACCAAATGCCGG	GCAACCTGAAGAATTACA 	:ggcctctccagggaaggt 	GTTGTGCCGTTTTTTCACTATTGTAGTCATCCTTG 	GTTTCATTCTGATATATATTTTCTCATT 	CCGCGGGAAATGCGTTAGTGTCAC CGCGGGGAAATGCGTTAGTGTCAC	CTCCATGAGTGAGAGAGATAGCTGGAT	TTCTCTCTCCTGCGC	AAGGACTCCTCGTAC AAGGACTCCTCTCGTAC	gcgcgggccggcrcgg 	acgcggganggcgacgttcgcggt 	
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	3157	2099	3097	2039	1979	2977	1919	2917	1859	2857	1799		1739	2737	1679	2677	1619	2617		2557	1499	2497	1439	2437	1379	2377	1319	2317	1259

RESULT 2
US-10-434-893A-1
; Sequence 1, Application US/10434893A
; Publication No. US20040060083A1
; GENERAL INFORMATION:
; APPLICANT: Ahmed Regina
; APPLICANT: Matthew Kennedy Morell
; APPLICANT: Sadequr Rahman

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RESULT 3
US-10-434-893A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 2780
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10434893A publication No. US20040060083A1 GENERAL INFORMATION:
APPLICANT: Ahmed Regina
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CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 2.1
SEQ ID NO 1
LENGTH: 2554
                                                                                                                                                                                                                                                                                  Matches 140;
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 93.(
Matches 211; Conservative
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Matthew Kennedy Morell
APPLICANT: Sadequr Rahman
ITITLE OF INVENTION: Barley with altered branching enzyme activity and starch and ITITLE OF INVENTION: containing products with an increased amylose content
FILE REFERENCE: 69425
CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT APPLING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTMARE: Patentin version 2.1
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TITLE OF INVENTION: containing products with an increased amylose content
FILE REFERENCE: 69425
                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: SSBEIIb cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: SSBEIIa cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                         Local Similarity
                                    1130
                                                                                                                                                                                                                              1010 GAAGTGAACATGACAGGGGGGACTGCAGAGAAACTTCAATCTTCAGAACCGACTCAGGGC 1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1002 AAACGGCGGAAGTGAACATGACAGGGGGGGACTGCAGAGAAACTTCAATCTTCAGAACCGA 1061
                                                                                                                                                                               298 GAACCAAGCCTGCACGATGGAGGTGAAGATACTATTCGGTCTTCAGAGACATATCAGGTT 357
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AAACCGCGAGTTGTCCCAAAACCAGGAGATGGGCAGAAATATACGAGATTGACCCAACA 1189
                                                                              ACTGAAGAAATTGATGCTGAAGGCGTGAGCAGAATGGACAAAGAATCATCCACGGTGAAG
                                                                                                                                ATTGTGGAAACAATCACTGATGGTGTAACCAAAGGAGTTAAGGAACTAGTCGTGGGGGAG 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCCAACACTGAAAGATTTTCGGAGCCATCTTGACTACCGGTAATGC 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGGGGAGAAACCGCGAGTTGTCCCCAAAACCAGGAGATGGGCAGAAAAATATACGAGATTG 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCCAACGCTGAAAGATTTTCGGAGCCATCTTGACTACCGATACAGC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCAGGGTATTGCGGAAACAATCACTGATGGTGTAACCAAAGGAGTTAAAGAACTAGTCG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGGGGAAAACCGCAAGTTGTCCCAAAACCAGGAGATGGGCAAAAAATATACGAGATTG
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Pred. No. 2.9e-15;
0; Mismatches 82;
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Pred. No. 3.6e-48; 
0; Mismatches 16;
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US-09-792-127-3
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10434893A Publication No. US20040060083A1 GENERAL INFORMATION:
                                                                                                                                                       SOFTWARE: PatentIn version 2.1 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
SEQ ID NO 3
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Best Local Similarity 61.3%;
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Patent No. US20020002713A1
                                                                                                                                                                                                 TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and starent of INVENTION: containing products with an increased amylose content FILE REFERENCE: 69425
CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ahmed Regina
APPLICANT: Matthew Kennedy Morell
APPLICANT: Sadegur Rahman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Starch Branching Enzyme FILE REFERENCE: B81439 US NA CURRENT APPLICATION NUMBER: US/09/792,127 CURRENT FILING DATE: 2001-02-23 PRIOR APPLICATION NUMBER: 60/186098 PRIOR FILING DATE: 2000-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Allen, Steve APPLICANT: Beckles, Diar APPLICANT: Butler, Karla APPLICANT: Pearlstein, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3039
TYPE: DNA
ORGANISM: Triticum aestivum
  NAME/KEY: MISC_FEATURE LOCATION: (1)...(6550)
                                                                           TYPE: DNA ORGANISM: Aegilops tauschii
                                                         FEATURE
                                                                                                                                ENGTH: 6550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1010 GAAGTGAACATGACAGGGGGGAGACTGCAGAGAAACTTCAATCTTCAGAACCGACTCAGGGC 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1190 CTGAAAGATTTTCGGAGCCATCTTGACTACCGGTAATGCCTA 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1130 АААСССССВАСТТСТСССААЛАССАССВОВЛЕССВОВАЛАТАТАССВОВТЕСЯСССВАСВ 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1070 ATTGTGGAAACAATCACTGATGGTGTAACCAAAGGAGTTAAGGAACTAGTCGTGGGGGAG 1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         552 CTCCGAGACTTTAAGTACCATCTTGAGTATCGATATAGCCTA 593
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Butler, Karla
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Pred. No. 2.5e-13;
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APPLICANT: Beckles, Diane M.
APPLICANT: Beckles, Diane M.
APPLICANT: Beckles, Rarla
APPLICANT: Pearlstein, Rich
TITLE OF INVENTION: Starch Branching Enzyme III
FILE REFERENCE: BB1439 US NA
CURRENT APPLICATION NUMBER: US/09/792,127
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/186098
PRIOR FILING DATE: 2000-03-01
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Microsoft Office 97
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Best Local S
Matches 81
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Best Local :
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                                   Sequence 130848, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2559
TYPE: DNA
ORGANISM: Triticum aestivum
-09-792-127-1
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CANT: Zhou Yihua
CANT: Cao Yongwei
CONT: Capt Congwei
COF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
COF INVENTION: Plants and Uses Thereof for Plant Improvement
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                                                                                                                                                                                                                                                                                              1183 CCCAACACTGAAAGATTTTCGGAGCCATCTTGACTACCGGTAATGCCTA 1231
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Similarity 61.4%;
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Pred. No. 2e-12;
0; Mismatches
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Pred. No. 2.2e-07;
0; Mismatches 28;
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GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
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SEQ ID NO 130848
LENGTH: 470
TYPE: DNA
                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 337
LENGTH: 2577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 337, Application US/09938842A Patent No. US20020160378A1
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CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                   Matches
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ŠTRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: PAT_MRT3847_89163C.1
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                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                 Local Similarity
nes 76; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 TTTTGCACTTTTGATACCTACTATACTGTAAATTTATAACGTAAATTTTTTAAAATGCTA
                                                                                                          1619 ACAGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATTGG 1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 TTTTTTAAATCACAGTTATGGACAATACAAAAGATTGCGTTATGAAATTGACAAGCATGA
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                                   AAGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCCGCAG
                                                                            ACCGATATGGGCAGTACAGAAAACTGCGTGAAGAAATTGACAAGAATGAAGGTGGTTTGG
   AGGCATTTTCTCGTGGTTATGAAATATTTGGCTTCACTCGAAG
                                                                                                                                                   Conservative
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Pred. No. 9.2e-08;
0; Mismatches 74
                                                                                                                                                     0;
                                                                                                                                                     Score 59.8; DB 9;
Pred. No. 4.5e-06;
0; Mismatches 27;
                                                                                                                                                                                           Length 2577;
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-337
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; Sequence 337, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-056-454A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3 CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-05-22 NUMBER OF SEQ ID NOS: 5379 SEQ ID NO 337 LENGTH: 2577 PRIOR APPLICATION NUMBER: US 60/300,111 PRIOR FILING DATE: 2001-06-22 NUMBER OF SEQ ID NOS: 5379 SEQ ID NO 337 LENGTH: 2577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
                                                                                                                 APPLICATION NUMBER: US/10/056,454A FILING DATE: 25-Jun-2002 INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: National Starch and Chemical Investment Holding Corporation TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1619 АСАGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATTGG 1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   587
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   527 ACCGATATGGGCAGTÁCAGAAAACTGCGTGAAGAAATTGACAAGAATGAAGGTGGTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                    STATE: Delaware COUNTRY: United States of America ZIP: 19720
                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Newcastle
                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                             LENGTH: 3231 base pairs
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5. US20040009476A9
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  DESCRIPTION: SEQ ID NO: 18:
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Pred. No. 4.5e-06;
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 130849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 130849, Application US/10424599
Publication No. US20040031072A1
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                                                                                                                                                             Matches
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-424-599-130849
                                                                                                                                                                                                                                                                                              LENGTH: 5164
TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1679 AAGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
                                 1680 AGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
                                                                                                                   1620 CAGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATTGGA 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                814 ACAGGTATTCACAGTACAAGAAÁATGAGGGAGGCAÁTTGACAAGTATGAGGGTGGTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  874 AAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAG 916
                                                                             927 CCGTTATGGACAATACAAAAGATTGTGTTATGAAATTGACAAGCATGAAGGCGGTCTGGA
987 TACATTTTCTCGTGGTTATGAAAAATTTGGCTTCATACGCAG
                                                                                                                                                                              2.7%;
Similarity 73.5%;
                                                                                                                                                           Conservative
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                                                                                                                                                           Score 58.8; DB 12;
Pred. No. 1.5e-05;
0; Mismatches 27;
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0; Mismatches 27;
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RESULT 12
US-10-397-954A-1
(Sequence 1, Application US/10397954A)
(Sequence 1, Application US/10397954A)
(Sequence 1, Application US2030221220A1)
(Publication No. US2030221220A1)
(GENERAL INFORMATION:
APPLICANT: Pearlstein, Richard W.
APPLICANT: Broglie, Karen E.
APPLICANT: Hines, Christopher F.
APPLICANT: Hines, Christopher F.
APPLICANT: Hines, Christopher F.
APPLICANT: Naize Starch Containing Elevated Amounts of Actual Amylose
FILE REFERENCE: BB1510 US NA
CURRENT APPLICATION NUMBER: US/10/397,954A
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: 60/368,387
PRIOR APPLICATION NUMBER: 60/368,387
PRIOR APPLICATION NUMBER: 60/368,387
PRIOR APPLICATION NUMBER: 60/368,387
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 60/381,534
PRIOR FILING DATE: 2002-05-16
SOPTWARRE: Microsoft Word 97
SEQ ID NO 1
LENGTH: 2443
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
NAME/KEY: misc_feature
LCCATION: (1).-(2443)
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Query Match

2.8%;

Score 59.8;

DB 14;

Length 3231;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature; LOCATION: (1)..(2443)
OTHER INFORMATION: SBEII modified region
US-10-397-954A-1
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Publication No. US20030221220A1
GENERAL INFORMATION:
APPLICANT: Pearlstein, Richard W.
APPLICANT: Broglie, Karen E.
APPLICANT: Hines, Christopher F.
TITLE OF INVENTION: Maize Starch Containing
FILE REFERENCE: BB1510 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 74.0
74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 2
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CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: 60/368,387
PRIOR FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 6
SOFTWARE: Microsoft Word 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/381,534
PRIOR FILING DATE: 2002-05-16
                                                                                                                              GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                         1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1622 GATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATTGGAAG 1681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1622 GATACAGCGAATACAAGAGAATTCGTGCTGCTATTGAACATGAAGGTGGATTGGAAG 1681
                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniquema Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTACAGCCTCTATAGAAGAATCCGTTCAGACATTGATGAACATGAAGGAGGCTTGGAAG 477
                                                                                                                                                                                                                                                                                                                                                                              CATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
                                                                                                                                                                                                                                                                                                                                                                                                                  GGTACAGCCTCTATAGAAGAATCCGTTCAGACATTGATGAACATGAAGGAGGCTTGGAAG
                                                     CITY: Newcastle
STATE: Delaware
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READABLE FORM
                                   United States
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Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58.4; DB 15;
Pred. No. 1.1e-05;
0; Mismatches 26;
                                     of America
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Best Local S
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SEQUENCE DESCRIPTION: SEQ ID NO: US-10-056-454A-17
                                                                                                                                                                                                                                            ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-056-454A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1619 AÇAGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATTGG 1678
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: National Starch and Chemical Investment Holding Corportific OF INVENTION: Improvements in or Relating to Plant Starch NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1679 AAGCATTTTCTCGTTGGTTATGAAAAGCTTTGGATTTACCCGCAG 1721
                                                                                                                  1619 ACAGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATTGG 1678
                                                                             508 ACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75; Conservative
                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACAGGTATTCACAGTACAAGAAACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGG 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                   AAGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCTTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTCGTAG 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Newcastle
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Pred. No. 1.3e-05;
0; Mismatches 28
                                                                                                                                                                 Score 58.2; DB 14;
Pred. No. 1.3e-05;
0; Mismatches 28;
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Search completed: April 10, 2004, 20:07:30 Job time : 766.289 secs

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CA726861
LOCUS
DEFINITION
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JOURNAL
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AUTHORS
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1 (bases 1 to 623)

Tingey, S. V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Miao, G., Caraher, N. and Hanafey, M.K.

DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                     CA726861 623 bp mRNA linear EST 26-NOV-2002 wdelf.pk002.g8 wdelf Triticum aestivum cDNA clone wdelf.pk002.g8 5' end, mRNA sequence. CA726861 CA726861 GI:25448761
                                                                                                   Crop Genetics
E. I. DuPont d
                                                                                                                                                                                                                                                                                          Triticum aestivum
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                                                I. DuPont de Nemours and Company
Innovation Way, P.O. Box 6104, Newark,
el: 302-631-2602
ax: 302-631-2607
                 ill: Scott.V.Tingey@USA.dupont.
      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAO29212
CAO29212
CAO292130
CBC29365
CCC293065
BE590829
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BE590829
BC240653
BM368073
AV105653
AV105653
AV1056772
CCC07572
CCC07572
CCG340947
AQ864199
BE3407666
BZ732892
BZ732893
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CCG2199431
CCG173191
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CA500698 WHE4023 D
BM441043 EBed02 SQ
CB629365 OSIIEBOSI
CG421022 ZMMBBC0003
BQ754975 EBed02 SQ
BE590829 WHE0855 F
BU996927 H106F01r
AV913706 AV913706
BQ240653 TAE05014F
BM368073 EBed01 SQ
CG421433 PUHML71TD
CC607572 OGOBJ47TH
CC607572 OGOBJ47TH
CC607572 OGOBJ47TH
CC607572 OGAZECTO
CG4404047 OG3D139TV
AQ864199 IDED0022L
BZ407662 OGAZECTO
BG99131 3524 13
BC991317 950003D05
BU099131 3524 21
BZ732892 OGEDB15TM
BZ732892 OGEDB15TM
BZ732893 OGEDB15TM
BZ732893 OGEDB15TC
CC730667 OGFCX67TC
CC730667 OGFCX67TC
CC730667 OGFCX67TC
CC730667 OGFCX67TC
CC730667 OGFCX67TC
CC300534 OGMAC4TT
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BZ7747600 L194412.D
BZ7477600 L194412.D
BZ747662 A4476662
AJ476662 A4476663
BZ4471663 AA476663
BZ44716663 GGAAZ61TM
BM443964 EBEM09_SQ
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1098
                                                                                                             Unpublished (2002)

Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture an
195 Dafoe Rd, Winnipeg, MB, Canada R3T
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutter@agr.gc.ca
was cloned directionally, not all sequence were from the 5' end (same with Average insert size is >2.0 kb
Plate: 031 row: H column: 05
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                                                                                                    Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
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                                                                                                      primer: M13 Reverse.
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/tissue_type="endosperm"
/lab_host="DH10B"
               /organism="Triticum aestivum"
/mol type="mRNA"
/cultivar="Glenlea"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Triticum aestivum"

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clone="TaE05031H05R"
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Pred. No. 4e-40;
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                                                                                                                                                                                         Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 00

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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pollination)"
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                                                                                                          /db_xref="taxon:4565"
/clone="G750115P11"
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/cultivar="recital"
                                                                                                                                                                 organism="Triticum aestivum"
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Pred. No. 1.8e-39;
       Score 235; DB 14;
Pred. No. 1.9e-39;
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                       Length 604;
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EST 15-JUL-2003 G750115P11,

day after

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/dev_stage="5 days after anthesis"
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/clone_lib="TaE05"
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NotI; Site_2: MluI; mRNA obtained from wheat seeds of
cultivar Glenlea 5 days post-anthesis"
Length 483;
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978 AGATACCTGAAGATATCGAGGAGCAAACGGCGGAAGTGAACATGACAGGGGGGACTGCAG
                                                                                                                                                                                                                                                                           AGAAACTTCAATCTTCAGAACCGACTCAGGGCATTGTGGAAACAATCACTGATGGTGTAA 1097
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                                                    ATGGGCAGAAAATATACGAGATTGACCCAACACTGAAAGATTTTCGGAGCCATCTTGACT
                                                                                                                                                                CCAAAGGAGTTAAGGAACTAGTCGTGGGGGAGAAACCGCGAGTTGTCCCAAAACCAGGAG 1157
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ATGGGCAGAAATATACGAGATTGACCCAACGCTGAAAGATTTTCGGAGCCATCTTGACT
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/sub_species="vulgare" /db_xref="GABI:282656" /db_xref="GABI:282656" /db_xref="taxon:112509" /clone="HZ64I18" /clone="HZ64I18" /tissue_type="pericarp" /dev_stage="0-7 DAP (days after pollination)" /lab_host="XI10-Gold" /clone=lib="HZ" /cl	Tel: 039482-5522 Fax: 039482-5555 Fax: 039482-5555 Email: stein@ipk-gatersleben.de Insert Length: 412 Std Error: 0.00 Plate: 64 row: I column: 18 Seq primer: M13rev. Seq primer: M13rev. 1412 Source /organism="Hordeum vulgare subsp. vulgare" /mol type="mRNA" /culfivar="barke"	SOURCE Hordeum vulgare subsp. vulgare ORGANISM Hordeum vulgare subsp. vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum. REFERENCE 1 (bases I to 412) AUTHORS Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U. TITLE Barley ESTs from developing seeds JOURNAL Contact: Stein Nils Contact: Stein Nils Molecular Markers Group, Department Genbank Institute of Plant Genetics and Crop Plant Research (IPK) Correngatr. 3. 06466, Gatersleben, Germany	SULT 5 029212 CA029212 FINITION HZ64I18r HZ Hordeum vul 5-PRIME, mRNA sequence. CESSION CA029212 RSION CA029212 YWORDS EST.	Query Match Best Local Similarity 93.2%; Pred. No. 4.6e-37; Best Local Similarity 93.2%; Pred. No. 4.6e-37; Matches 234; Conservative 0; Mismatches 17; Indels 0; Gaps 0; 978 AGATACCTGAAGATATCGAGGAGCAAACGGCGAAGTGAACATGACAGGGGGACTGCAG 1037 pb 307 AGGTACCTGAAGATATCGAGGAGCAAATGGCGAAGTAAACATGACAGGGGGGACTGCAG 366 pb 307 AGGTACCTGAAGATATCTCAGACCGACTCAGGGCATTGTGGAAACAATCACTGATGGTGAA 1097 pp 1038 AGAAACTTCAATCTTCAGAACCGACTCAGGGCATTGTGGAAACAATCACTGATGGTGTAA 426 pb 367 AAAAACTTGAATCTTCAGAACCGACTCAGGGCATTTGCGGAAACAATCACTGATGGTGTAA 426 pp 1098 CCAAAAGGAGTTAAGGAACTAGTCGTGGGGAGGTATTGCGGAAACAATCACTGATGGTGTAA 426 pb 427 CCAAAAGGAGTTAAGGAACTAGTCGTTGGGGAGAAACCAAGTGCCCAAAACCAGGAG pb 487 ATGGGCAAAAATATACGAGATTGACCCAACACTGAAGATTTTCGGAGCCATCTTGACT 1217 pb 487 ATGGGCAAAAATATACGAGGATTGACCCAACACTGAAAGATTTTCGGAGCCATCTTGACT 546 Qy 1218 ACCGGTAATGC 1228 pb 547 ACCGATACACG 557

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RESULT 6
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Anderson,O.D., Chao,S., Crossman,C., Langridge,P., Lazo,G.R., Pham,J., Rausch,C.J., Sutton,T., Woo,J. and Wilson,C.
The structure and function of the expressed portion of the wheat genomes - Meiotic anther cDNA library
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EST.
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US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: oandersn@pw.usda.gov
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                /dev stages | Meiotic stages pre-meiosis-metaphase I" / lab_host="B. coli DH10B" / Clone_lib="Wheat meiotic anther cDNA library" / Clone_lib="Wheat meiotic anther cDNA library" / note="Vector: pspCRT1; Site_1: SalI; Site_2: NotI; Plants were grown in a glasshouse. Anther meiotic stage was determined by removing anthers from individual primary florets. One anther was sacrificed for microscopic staging, and if determined to be between (and including) meiotic stages pre-meiosis and metaphase I, the remaining two anthers were collected and pooled for library was mathers were collected and pooled for library two anthers were collected and pooled for library two and the library two anthers were collected and pooled for library two and the library two a
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Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk
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1 (bases 1 to 219)

Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L., Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R. Development of Barley Transcriptome Resources
Unpublished (2001)

On Feb 1, 2002 this sequence version replaced gi:18471818.

Contact: Waugh R, Marshall DF
Contact: Waugh R, Marshall DF
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                                                                                                                                                                                               /sub_species="vulgare"
/db_xref="taxon:112509"
/clone="EBed02_SQ002_E01"
/tissue_type="endosperm"
/dev_stage="8_DPA"
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 831)
Jantasuriyarat, C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Kudrna,D., Dean,R., Soderlund, C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A,
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Plate: 05 row: I column: 20
Seq primer: gta aaa cga cgg co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: http://genome.arizona.edu
PCR PRimers
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Fax: 520 621 9288
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BACKWARD: gga aac agc tat gac cat g
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/tissue_type="Lasf"
/tev stage="3 week"
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/lab host="PH10B"
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/mol_type="mRNA"
/cultivar="IR36"
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                                                                                                                                                                                                          db_xref="taxon:39946"
clone="OSIIEb05I20"
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Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A. Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003c)
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ZMMBBC0034G11f ZMMBBC (ECORI) Zea mays subsp. mays genomic
ZMMBBC0034G11 5', genomic survey sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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CG421022.1
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Class: BAC ends
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Fax: 732 445 5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dr.Joachim Messing's lab
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Bharti, A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2003)
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                                                                              Similarity
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                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                         bharti@waksman.rutgers
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                            /clone="ZMMBBc0034G11"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBc (EccRI)"
/note="Vector: pTARBAC2.1; '
                                                                                                                                                                                                                                           organism="Zea mays
/mol_type="genomic [
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:34565867
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EBed02_SQ003_F18_R endosperm, 8 DPA, no ti
Hordeum vulgare subsp. vulgare cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                     Invergowrie, Dundee, DD
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotlan
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                            est@scri.sari.ac.uk.
/sub_species="vulgare"
/db_xref="taxon:112609"
/clone="Ebed02_SQ003_F18"
/tissue_type="endosperm"
/dev_stage="8_DPA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 TCTGGGCGACTGGCTGAATCACTACGCGGG-GATGGCGACGTTCGCGGTGTCCGGC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D. Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the genomes - 20-45 DAP spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE590829 342 bp mRNA linear EST 18-AUG-2000
WHE0855_F05_K09ZS Wheat 20-45_DAP spike cDNA library Triticum
aestivum cDNA clone WHE0855_F05_K09, mRNA sequence.
                                                                                                                                                                                                                                                                             guality sequence with phred score less than Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                     Email: oandersn@pw.usda.gov
Sequence have been trimmed
                                                                                                                                                                                                                                                                                                                                                                                                    800 Buchanan Street, Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                        US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                               Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Olin Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pooideae; Triticeae; Triticum.
1 (bases 1 to 342)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cione_lib="endosperm,
EBed02"
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/clone="WHE0855_F05_K09"
/tissue_type="Spike and seed"
/dev_stage="Adult plant"
/lab host="E. col1 SCLR"
/clone_lib="Wheat 20-45 DAP spike cDNA library"
/clone_lib="Wheat 20-45 DAP XR, excised phagemid,
/note="Vector: Lambda Uni-ZAP XR, excised phagemid,
site_1: EcoRI; Site_2: XhoI; Plants were grown in t
greenhouse. Spikes at 20 DAP and seeds at 30 to 4
                                                                                                                                                                       /mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                             organism="Triticum aestivum"
                                                                                                                                                                                                                                                                        Location/Qualifiers
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87.9%;
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Pred. No. 1.6e-14;
0; Mismatches 17;
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ORIGIN

were harvested, total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

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RESULT 12
BU996927
LOCUS
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AUTHORS
TITLE
JOURNAL
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ORGANISM
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VERSION
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                                       ORIGIN
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Best Local Similarity
Query Match
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HI06F01r HI Hordeum vulgare subsp.
5-PRIME, mRNA sequence.
BU996927
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Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Eukaryota, Viridiplantae, Striptophyta, Embryophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Hordeum.
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: stein@ipk-gatersleben.de
Insert Length: 517 Std Error: 0.00
Plate: 6 row: F column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPX)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thang, H., Weschke, W., Michalek, W., Stein, N. EST sequencing and analysis in barley (2002) Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: Ml3rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Stein Nils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAAGCATTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG 1721
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                                                    /clone_lib="HI"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, Sall, PBtI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                     /tissue_type="female inflorescences"
/dev_stage="female inflorescences (approx. 3 mm in size)"
/_ab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                    /db xref="taxon:112509"
/clone="HI06F01"
                                                                                                                                                                                                                                                                                                                                            /sub_species="vulgare"
/db_xref="GABI:250791"
                                                                                                                                                                                                                                                                                                                                                                                    mol_type="mRNA"
cultivar="barke"
                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Hordeum vulgare subsp. vulgare"
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Pred. No. 1e-10;
0; Mismatches 3;
    Score
    98.6;
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vulgare
    멂
    13;
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cDNA clone HI06F01
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    517;
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VERSION KEYWORDS SOURCE

sequence. \$0240653 \$0240653.1 GI:20436529 EST. Triticum aestivum (bread wheat)

BQ240653 568 bp ml TaE05014F06R TaE05 Triticum aestivum

cDNA clone TaE05014F06R, mRNA

linear

EST 03-MAY-2002

ACCESSION DEFINITION

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KEYWORDS
SOURCE
ORGANISM
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AV913706
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Matches 101
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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                                                                                     81 GGAAGTTTTTCTCGTGGTTATGAAAAGCTTGGATTTACCCGCAG
                                                                                                                                                     21 CTACCGATACAGCGAATACAAGAGAATTCGTGCTGCTATTGACCAACATGAAGGTGGATT
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Hordeum vulgare subsp. vulgare
Botaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases 1 to 556)
Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         germination shoots Hordeum v
bags23a09 5', mRNA sequence.
AV913706
AV913706.1 GI:18209483
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Tadasu Shin-i
                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                      4.6%;
ilarity 96.2%;
Conservative
                                                                                                                                                                                                                                                                                                        /dev_stage="germination"
/clone_lib="K. Sato unpublished cDNA library, cv. Haruna
Nijo germination shoots"
                                                                                                                                                                                                                                                                                                                                                                        /sub_species="vulgare"
/db_xref="taxon:112509"
/clone="bags23a09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                               tissue
                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/cultivar="Haruna Nijo"
                                                                                                                                                                                                                                                                                                                                                             type="shoots"
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D; Mismatches 4
                                                                                                                                                                                                                          Score 98.6; DB 9;
Pred. No. 2.4e-10;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subsp. vulgare"
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, cv. Haruna Nijo
vulgare cDNA clone
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                                                                                  1 (bases 1 to 139)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: scloutier@agr.gc.ca
mas cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >2.0 kb
Plate: 014 row: F column: 06
                                                                                                                                                                                               Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland
                                                                                                                                                                                                                                                                                                                                                                                                            BM368073

139 bp mRNA linear EST 23-JUL-2002
EBed01_SQ002_B11_R endosperm, 6 DPA, no treatment, cv Optic, EBed01
Hordeum vulgare subsp. vulgare cDNA clone EBed01_SQ002_B11 5', mRNA
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                 Contact: Waugh R, Marshall DF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="TaE05"
/note="Vector: pspORT-p (Invitrogen Technologies); Site_1:
NotI; Site_2: MluI; mRNA obtained from wheat seeds of
cultivar Glenlea 5 days post-anthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="TaB05014F06R"
/tissue_type="developing seeds"
/dev_stage="5 days after anthes:
/lab_host="2. coli DH10B"
/clone_lib="TaB05"
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                                                                                                                                                                                                                                                                         161 GGTGTCCGGCGACTCTCGGTGTGGCGCGGGCGGGCCGGCGTCGGAG----TGGCGCGGGCCGG 217
                                                                               121 TCG 123
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                                                                                                                                                                                                                                                 GETETCCGGCGACCCTTGGTGTGGCGCGGGGGCCGCCGGCGAGCGCTGCCGCGATCCGG
                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="endosperm, 6 DPA, no treatment, cv Optic. \mathtt{EBed01}^{\mathrm{m}}
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Pred. No. 3.7e-09;
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length: 2000000000
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Copyright (c) 1993 - 2004 Compugen Ltd.
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AUTHORS
TITLE
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                                                                                                                            Sequence 10 from Patent WO9914314.
                                        Aegilops tauschii
Aegilops tauschii
Eukaryota, Viridiplantae, Streptophyta, Empryophyta, Tracheophyta,
Eukaryota, Viridiplantae, Liliopsida, Poales, Poaceae,
Spermatophyta, Magnoliophyta, Liliopsida, Poaceae,
Pooideae, Triticeae, Aegilops.
    Li, Z., Morell, M. and Rahman, S. Regulation of gene expression
                                                                                                                      AX031271.1
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GI:10278603

DNA

linear

PAT 20-SEP-2000

in plants

ALIGNMENTS

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	U	% Query Match	Length	₽B	ID	scriptio	_
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4 5		_		œ	Y29026	290265	ea may
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6618 CHACGAGTCTTAGATAGTTCCTTAGTTGCTTGTACATTTTACCTGATGAGATCATGG 6677 1861 AAGATTGGAAGTGATTATTATTTATTTCTTTCTTAGTTTCTTGTTCTTAGATGACA 1920	TGGCACTACATAGAGT 840	y 721 CATAGAATATCGTTTGTAATGCAACACAATTTCATGCCAAGAGATGGAAGGT	\$ B \$
	720 5537	661 A 5478 A	dd 40
498 ACCTCCATGATGTATACTCACCATGGAT	C 660 C 5477	601 G 5418 G	Qy Db
438	600 5417	Y 541 AAGGAAAATTGGCAAAAACTAGAGTGGCAAAAATAAAAT	Qy dd
378	540 5357	481 ATGATACATTGTCAAAAGCTAAGAGTGGCGAAAGTGAAATGT	dd Yo
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15 5 15 63	TTATGGATATTGTTCATAGGTAATTAGTC 420	361 GATAGAGCACATGAGCTTGGTTTGCTTGTTC	dd YQ
	C 360 C 5177	301 ACTAATTTTTTGCACCAAGTAGCCGTTTTGGAACTC	dd Ad
1381 GCAGTCATTCGTCAAATAATACCCTTGACGGTTGAATGGTTTCGATGGCACTGATACAC 14	300	241 ACACTTAGTATTCTGAAAAAGATCATTTTATTGTTG	4d 70
078 TETTTGGTTAGCCACTTGCTTTCATATTTATGTGTTCATCATGATGTATTTGTGTACCTTATCTTCCTTC	TCCTTTATTAGATATATAGTACAACT 240	181 TAATGCTTCATGCACATAAAATATTTGGATATAA	qq
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	4877	1 CCGAAGATAAATTCATATGCTAATTTTAGGGATGAGGTGTT 	QY
021 TACAACACCAAATTACTTTGATCAGATTAACAATTTTTATTTTATTATATATA	Length 11463; Oy Indels 0; Gaps 0;	the structure of Match (Conservative Of Mismatches Of I tocal Similarity 100.0%; Pred. No. 0; I tohes 2050; Conservative Of Mismatches Of I	Que Ber Mat
961 TTTGTCCTAAGTCAAACTTCTTTAAGTTTGACCAAGTCTATTGGAAAATATATAT	STARCH BRANCHING ENZYME Db	#ISC_feature 1. 11453 /product="COMPLETE SEQUENCE OF THE II GENE"	
901 TTCATACTAGAIGTTACTTCCCTGTTGAATTCATTTGAACATATTACTTAAAGTTCTTCA 960 	Qy dd	/organism="Aegilops tauschii" /organism="Lopse tauschii" /mol_type="unassigned DNA" /db_xref="taxon:37682"	
5598 TCAGATGCTATCAATAGAATTAATCAACTGGCCATGTACTGGGCACTACATATAGTTT 5657 841 GCAAGTTGGAAAACTGACAGCAATACCTCACTGATAAGTGGCCAGGCCCCACTTGCCAGC 900	MORELL MATTHEW (AU); COMMW SCIENT IND RES Db	Patent: WO 9914314-A 10 25-MAR-1999; GOODMAN FIELDER LTD (AU); LI ZHONGYI (AU); RAHMAN SADEQUR (AU); UNIV AUSTRALIAN (AU); ORG (AU); GROUPE LIMAGRAIN PACIFIC PTY L (AU Location/Qualifiers	JOI FEATI
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TTTACTGGGAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGATGCGGTAGTTTAC 1980

TTTACTGGGAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGATGCGGTAGTTTAC 6797

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RPRSFSVYTPSRTAVVYALTE"

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PUBMED
REFERENCE
AUTHORS
TITLE
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rahman,S., Regina,A., Li,Z., Mukai,Y., Yamamoto,M.,
Kosar-Hashemi,B., Abrahams,S. and Morell,M.K.
Comparison of starch-branching enzyme genes reveals evolutionary
relationships among isoforms. Characterization of a gene for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Foales; Poaceae; Pooideae; Triticeae; Aegilops.

1 (bases 1 to 11475)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aegilops tauschii starch branching enzyme IIa gene, AF338431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (18-JAN-2001) Plant Industry, CSIRO, Clunies Ross,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rahman, S., Regina, A., Li, Z., Sharon, A. and Morell, M.K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              starch-branching enzyme IIa from the wheat genome donor Aegilops
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                  Physiol. 125 (3), 1314-1324 (2001)
                                                                                                                                                                                                                                                                                                                             join(<1204. 1336,1664. 1761,2038. .2279,2681. .2779, 2949. .2941,3144. .3203,3539. .3619,3703. .3819,4105. .4188, 4818. .4939,5115. .5234,6209. .6338,6427. .6537,6739. .6867,7447. .7550,3392. .8536,556. .9703,8839. .9939,10116. .10193, 10395. .10550,10928. .11002,11092. .11475)
/product_"starch branching enzyme IIa"
join(1204. .1336,1664. .1761,2038. .2279,2681. .2779, 2681. .2779, 2681. .2779, 2681. .2739, 2681. .2739, 2681. .2739, 2681. .2739, 2681. .2739, 2681. .2739, 2681. .2389,43703. .3819,4105. .4188, 43818. .4393,5115. .5230,3539. .3619,3703. .8687, 7447. .7550,8392. .8536,9556. .9703,9839. .9339,10116. .10193, 10395. .001974. .10193, 10395. .10550,10928. .11002,11092. .11175)
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Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae; PACCAD
Spermatophyta; Magmoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E. Genetic diversity and selection in the maize starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
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Zea mays subsp. m
starch-branching
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277. .387
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Oy 1883 TATTTTCTTAAGTTTGTTTCTTGTTCTAGATGACATTTACTGGGAACTATGGCGAAT 1942 Db 521TGCATTTTACTTAGATAACTATTACGGGAACTTCAATAAT 563	University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA Location/Qualifiers .e 1. 693	
	rect Submission bmitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina Sta	II O
QY 1823 CTAGTATGCTTGTACAATTTTACCTGATGAGATCATGGAAGATTGGAAGTGATTATTATT 1882	REFERENCE 2 (bases 1 to 693) AUTHORS Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.	AU
AGTCTGACTGGAATACTGGATTATGCCTGGGAACTAGTTTTGTTTAGTATC	22247734	M M
Db 377 ACGGATTACAAGTAATTTAAGCTTIATGCCTGTTAGTTTATTCTTCACTTGCTA 429	AUTHORS Whitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S. and Buckler, E.S. TITLE Genetic diversity and selection in the maize starch pathway TOTRMAIL BOOK MALE AND 18 & 00 (20) 10860-10862 (2002)	T A
ATGGATTACAAGTAAGTCATCAAGTGGTTTCAGTAACTTTTTTAGGGCACTGAAACAATT	openmerophyra, magnotarophyra, marcystra, roases, forcese, forces clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 693)	REFEI
QY 1643 AAGAATATAAGTITGATGGATTTCGATTTGATGGGGTGACCTCCATGATGTATACTCACC 1702	SOURCE Zea mays subsp. mays (maize) ORGANISM Zea mays subsp. mays Eukaryote, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Coordan Manager, Viridiplantae; Illipopids, Doslag, Doscos, Daffin	SOUR
Db 257 ACAATTTATCCGTATGCAGGTTTTAAGATTTCTTCTCTCCAATGCTAGATGGTGGCTCG 316	VERSION A1235591.1 GI:30014005 EXPMORDS	VERS
Qy 1583 GATATTCTATTCTTATGCAGGTATTGAGATTCTTACTGTCAAACGCGAGATGGTGGCTTG 1642	Zea mays subsp. mays cultivas enzyme (ael) gene, exons 12, av235601	DEFI.
Qy 1523 CICTGACTTCTGTCACCATATTTGGCTAACTGTTCCTGTTAATCTGTTCTTACACATGTT 1582	693 bp DNA linear	RESU AY23 LOCU
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QY 1403 CCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACATTACTTCCACGGTGGTCCACG 1462	QY .1943 ATTITGGATTITGCTACTGATGTTGATGCTGGTTGATGCTACGATCTAA 2002	유 양 호
Qy 1343 TICAGTIGCATIGCITCAAIGATTIGTGIACCCIGCAGTCAITCGICAAATAAIAC 1402	521	Db
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y Match 12.2%; Score 250.8;		γ
/genc /numl	430 AGTCTGACTGGAATACTGCGTGGGAACTAGTTTTGTTTAGTATC	Db 45
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LRFLLSNARWMLEEYKFDGFREDGVTSMMYTHHGLQVTFTGNFNEYFGFATDVDAVV LMLVNDLIHGLYFEAVTIGEDV" 6xon 61. 190	QY 1643 AAGAATATAAGTTTGATGGATTTCGATTTGATGGGGTGACCTCCATGATGTATACTCACC 1702	A A
/procern_respectively.com /db_xref="GI:30014006" /translation="HASSNTLDGLNGFDGTDTHYFHSGPRGHHWMWDSRLFNYGNWE	Db 257 ACAATTTTATCCGTATGCAGGTTTTAAGATTTCTTCTCCCAATGCTAGATGGTGGCTCG 316	핝
<pre>/codon_start=2 /product="amylose extender starch-branching enzyme" /profein id="mappnag43 1"</pre>	1583 GATATTCTATTCTATGCAGGTATTGAGATTCTTACTGTCAAACGCGAGATGGTGGCTTG	γo
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/sub_spec /db_xref=	79 TCTGGATGGGTTGAATGGTTTTTGATGGTACAGATACATTACTTTCACAGTGGTCTAT) 말
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Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
Genetic diversity and selection in the malze starch pathway
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
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                                                                                                        Conservative
                                                                                                                                                                                                             536. .668
/gene="ael"
/number=14
                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="hassntldglngfdgtdthyfhsgprghhmmmdsrlfnygnwev
lrfllsnarwwleeykfdgfrfdgvtsmyythhglqvtftgnfneyfgfatdvdavvy
                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="amylose extender starch-branching enzyme/
protein ide"AAP03853,1"
/db_xref="GI:30014026"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Juin(<61. .190,277. .387,536. .>668)
/gene="ae1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sub_species="mays"
/db_xref="taxon:4578"
                                                                                                                                                                                                                                                                         'number=13
                                                                                                                                                                                                                                                                                         'gene="ae1"
                                                                                                                                                                                                                                                                                                                                                                                                   "MLVNDLIHGLYPEAVTIGEDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="ael"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product="amylose extender starch-branching enzyme"
join(<61. .190,277. .387,536. .>668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="ae1"
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                           gene="ae1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=2
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                                                                                                                         12.2%;
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                                                                                                                         Score 250.8; DB 8; Pred. No. 1.7e-40;
                                                                                                        Mismatches
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x 7614, Raleigh,
                                                                                                        192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaut, B.S.
                                                                                                                                             Length 693;
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carolina State
NC 27695, USA
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                                                                                                        55.
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AUTHORS
TITLE
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AY235702
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Submitted (13-FEB-2003) Genetics, USDA-ARS, North University, 3513 Gardner Hall, Box 7614, Raleigh, Location/Qualifiers
                                                                                                                                                                                                           1 (bases 1 to 712)
Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
                                                                                                                                                                                                                                                                                         Zea mays subsp. mays (maize)
Zea mays subsp. mays
Zea mays subsp. mays
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY235702 712 bp DNA linear Zea mays subsp. mays cultivar I205 amylose extender starch-branching enzyme (ael) gene, exons 12, 13, ar
                                                                                    Direct Submission
                                                                                                                           Whitt, S.R.,
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                                                                                                                                               (bases 1 to 712)
                                                                                                                           Wilson, L.M.,
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                                                                                                                           Tenaillon, M.I.,
                                                                                                                           Gaut, B.S.
                                          Carolina State
NC 27695, USA
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                                                                                                                           and Buckler, E.S.
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623

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376 1702 316 256

196

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Matches 461;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTGACTTCTGTCACCATATTTGGCTAACTGTTCCTGTTAATCTGTTCTTACACATGTT
TATTTTCTTTCTAAGTTTGTTTCTTGTTCTAGATGACATTTACTGGGGAACTATGGCGAAT 1942
                                                                            CTAGTATGCTTGTACAATTTTACCTGATGAGATCATGGAAGATTGGAAGTGATTATTATT 1882
                                                                                                                                                      GCTATGCATCATAACATGTATCATGATCAGGACTTGTGCTACGGAGTCTTAGATAGTTCC 1822
                                                                                                                                                                                                                                                                                                  AAGAATATAAGTTTGATGGATTTCGATTTGATGGGGTGACCTCCATGATGTATACTCACC
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277. .387
/gene="ae1"
/number=13
536. .668
/gene="ae1"
/number=14
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/protein id="AAP03854.1"
/dbxref="G1:30014028"
/translation="HASSNTLOGLNGFDGTDTHYFHSGFRGHHWMWDSRLFNYGNWEV
/translation="HASSNTLDGLNGFDGTDTHYFHSGFRGHFNEYFGFATDVDAVVY
LRFLLSNARWWLEEYKFDGFRFDGVTSMMYTHHGLQVTFTGNFNEYFGFATDVDAVVY
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/gene="ae1"
/product "amylose extender starch-branching
join(<61..190,277..387,536..>668)
/gene="ae1"
/codon_start=2
/codon_start=2
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/mol_type="genomic DNA"
/cultivar="I205"
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Pred. No. 1.7e-40;
0; Mismatches 192;
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AY235690
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mays subsp. mays (maize)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
close; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State
University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
Location/Qualifiers
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Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
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Whitt,S.R., Wilson,L.M.,
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12.2%;
ilarity 65.1%;
Conservative
                                                                                                /number=12
277.387
/gene="ae1"
/number=13
536.668
/gene="ae1"
/number=14
                                                                                                                                                                                                                                                                                            /codon_start=2
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LRFLLSNARWWLEEYKFDGFRFDGVTSMMYTHHGLQVTFTGNFNEYFGFATDVDAVVY
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/gene="ae1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
/cultivar="A272"
                                                                                                                                                                                                                                                                                                                                                                                                                                       product="amylose extender starch-branching oin(<61. .190,277. .387,536. .>668)
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Score 250.8; DB 8;
Pred. No. 1.7e-40;
0; Mismatches 192;
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                                         Length
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AY235692
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Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 713)
Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
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Zea mays subsp. mays cultivar B103 amylose extender
starch-branching enzyme (ael) gene, exons 12, 13, an
                                                  2 (bases 1 Whitt,S.R.,
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Wilson, L.M.,
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Location/Qualifiers
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                    ATATTTGTTATATATCATTCCTTCTTCTAATCTAAAGTCA
                                                        CTAGTATGCTTGTACAATTTTACCTGATGAGATCATGGAAGATTGGAAGTGATTATTATT 1882
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nilarity 65.1%;
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/gene="ae1"
/number=14
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/number=13
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277. .387
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Lrfllsnarmmleeykfdgfrfdgvtsmmythhglqvtftgnfneyfgfatdvdavvy
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join(<61. .190,277. .387,536. .>668)
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/gene="ael"
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/db_xref="taxon:4578"
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/mol_type="genomic DNA"
/cultivar="B103"
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Pred. No. 1.7e-40;
0; Mismatches 192;
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Query M Best Lo	ORIGIN	exon	exon	exon	CDS	gene mRNA		TITLE JOURNAL FEATURES source	JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 9 AY235693 LOCUS DEFINITION	OY OB	Q dd A
Match 12.2%; Score 250.8; DB 8; Length 713;		/number=13 536668 /gene="ae1" /number=14	/gene="ae1" /number=12 277. 387 /gene="ae1"	/codon_start=2 /product="amylose extender starch-branching enzyme" /product="amylose extender starch-branching enzyme" /product="alaP03845.1" /db_xref="GI:30014010" /translation="HASSNTLDGLNGFDGTDTHYFHSGDRGHHWWWDSRLFNYGNWEV LRFLLSNARWWLEEYKFDGFRFDGVTSMYYTHHGLQVTFTGNFNEYFGFATDVDAVVY LMLVDDLHGLYPEAVTIGEDV" 61190	/gene="ael" /product="amylose extender starch-branching enzyme" join(<61190,277387,536>668) /gene="ael"	115.0	<pre>/organism="Zea mays subsp. mays" /mol type="genomic DNA" /cultivar="B14A" /sub species="mays" /db xref="taxon:4578"</pre>	0	Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12982 (2002) 22247734 12244216 2 (bases 1 to 713) Whitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S. and Buckler, E.S.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta Spermatophyta; Magnollophyta; Liliopsida; Poales; F clade; Panicoideae; Andropogoneae; Zea 1 (bases 1 to 713) Nhitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S. Genetic Aiversity and Reslection in the maize strack	partial ods. AY235693 AY235693.1 GI:30014009 Zea mays subsp. mays (maize) Zea mays subsp. mays	AY235693 713 bp DNA linear PLN 1 Zea mays subsp. mays cultivar B14A amylose extender	564 ATTTTGCCTTTGCCACGATGTAAAIGAGTGGTTTACTTGATGCTGGTAAAIGATCTAA 623 2003 TTCATGGACTTTATCCTGATGCTGTATCCATTGGTGAAGATGTAAGTG 2050	1883 TATTITCTITCTAAGTITGTITCTGTICTAGATGACATTTACTGGGAACTATGGCGAAT 1942 521TGCATTTTACTTTAGGTAACATTTACGGGAACTTCAATGAGT 563 1943 ATTITGGATTTGCTACTGATGTGATGCGGTAGTTTACTTGATCTAACGATCTAA 2002
AUTHORS Wiltt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.	PUBMED 12244216	Whitt, S.R., Wilson, L.M., Tenaillon, M.I., G Genetic diversity and selection in the mai Proc. Natl. Acad. Sci. U.S.A. 99 (20), 129 22247734	Eukaryota; Viridipiantae; Spermatophyta; Magnolioph clade; Panicoideae; Andro 1 (bases 1 to 713)	AY235694 Illear PLN 16-APK-2 N Zea mays subsp. mays cultivar B37 amylose extender starch-branch enzyme (ael) gene, exons 12, 13, and 14 and partial cds. AY235694 AY235694.1 GI:30014011 Zea mays subsp. mays (maize) N Zea mays subsp. mays		Qy 2003 TTCATGGACTTTATCCTGATGCTGTATCCATTGGTGAAGATGTAAGTG 2050	QY 1943 ATTITGGATITGCTACTGATGTGATGCGGTAGTTTACTTGATGCTGGTCAACGATCTAA 2002	Db 481 ATATTTGTTATATATCATTCCTTCTAATCTAAAGTCA	QY 1763 GCTATGCATCATAACATGTATCATGATCAGGACTTGTGCTACGGAGTCTTAGATAGTTCC 1822	Db 317 AGGATTATAAGTTTGATGGTTTTGATGGTGTAACCTCCATGATGTACACTCATC 376 Qy 1703 ATGGATTACAAGTAAGTCATCAAGTGGTTTCAGTAACCTTTTTTAGGGCACTGAAACAATT 1762	1583 GATATTCTATTCTTATGCAGGTATTGAGATTCTTACTGTCAAACGCGAGATGGTGGCTTG	Db 139 TĠĠĊĀTĊĀCTĠĠĀTĠTĠĠĀTTĊŤĊĠĊĊŤĀTTTĀĀĊTĀTĠĠĀACTĠĠĠĀĀĞTĀCGĠ 196 Qy 1523 CTCTGĄCTTCTGTCĄCÇATATTTGGCTAACTGTTCCTGTTTACACATGTT 1582	OY 1403 CCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACATTACTTCCACGGTGGTCCACG 1462	Matches 461; Conservative 0; Mismatches 192; Indels 55; Gaps 4; Qy 1343 TTCAGTTGCATTCATCATCATGATTTTGTGTACCCTGCAGTCATTCGTCAAATAATAC 1402

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Submitted (13-FEB-2003) Genetics, USDA-ARS, North
University, 3513 Gardner Hall, Box 7614, Raleigh,
Location/Qualifiers
                                                                                                                                                                                                                     AAGAATATAAGTTTGATGGATTTCGATTTGATGGGGTGACCTCCATGATGTATACTCACC
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               CTAGTATGCTTGTACAATTTTACCTGATGAGATCATGGAAGATTGGAAGTGATTATTATT 1882
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                                                     AGTCTGACTGGAATACTGGATTATGCCTGGGAACT----AGTTTTGTTTAGTATC
                                                                                       GCTATGCATCATAACATGTATCATGATCAGGACTTGTGCTACGGAGTCTTAGATAGTTCC
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LRFLLSNARWWLEEYKFDGFRFDGVTSMMYTHHGLQVTFTGNFNEYFGFATDVDAVVY
LMLVNDLIHGLYPEAVTIGEDV"
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/db_xref="GI:30014012"
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0; Mismatches 192; Indels
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University, 3513 Gardner Hall, Box 7614, Raleigh,
Location/Qualifiers
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Whitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S. and Buckler, E.S. Generic diversity and selection in the maize starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
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Whitt,S.R., Wilson,L.M.,
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                                                   536. .668
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NC 27695, USA
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RESULT 12
AY235696
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AUTHORS
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VERSION
KEYWORDS
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ORGANISM
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12244216
2 (bases 1
Whitt,S.R.,
                                                                                                                                                                                                                                Zea mays subsp. mays cultivar B97 amylose extender starch-branching enzyme (ael) gene, exons 12, 13, and 14 and partial cds.
AY235696
AY235696.1 GI:30014015
                                                                                                                                         Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                 hitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S. and Buckler, B. Genetic diversity and selection in the maize starch pathway proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
                                                                                                                                                                                                             Zea mays subsp. mays (maize)
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to 713)
Wilson, L.M.,
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0; Mismatches 192;
Tenaillon, M.I.,
 Gaut, B.S.
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and Buckler,
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Direct Submission
Submitted (13-FEB-2003) Genetics, USDA-ARS, North
University, 3513 Gardner Hall, Box 7614, Raleigh,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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     CTAGTATGCTTGTACAATTTTACCTGATGAGATCATGGAAGATTGGAAGTGATTATTATT
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ilarity 65.1%;
Conservative
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/number=13
536. .668
/gene="ae1"
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277. .387
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/gene="ae1"
/codon_start=2
/poducte-mmylose extender starch-branching enzyme"
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/protein_id="AAP03848.1"
/db xref="GI:30014016"
/tanslation="HASSYTLDGLNGFDGTDTHYFHSGPRGHHWMWDSRLFNYGNWEV
/translation="HASSYTLDGLNGFDGTDTHYFHSGPRGHHWMWDSRLFNYGNWEV
LRFLLSNARWWLEEYKFDGFRFDGVTSMMYTHHGLQVTFTGNFNEYFGFATDVDAVVY
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join(<61..190,277..387,536.
/gene="ae1"
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join(<61. .190,277. .387,536. .>668)
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/db_xref="taxon:4578"
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/mol_type="genomic DNA"
/cultivar="B97"
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pred. No. 1.7e-40;
0; Mismatches 192;
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exon exon exon ORIGIN	CDS	gene mRNA	TITLE JOURNAL FEATURES source	ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	RESULT 13 AY235697 LOCUS DEFINITION DEFINITION VERSION VERSION KEYWORDS	Db 4 Qy 18 Db 5 Qy 19 Qy 19 Db 5 Qy 20 Qy 20
IRFILSUARAWMIESTREDGVISMMYTHHGLQVIFTGNEWEYFGFATDVDAVVY LMLVNDLIHGLYPEAVTIGEDV" 61190 /gene="ae1" /number=12 277.387 /gene="ae1" /number=13 536668 /gene="ae1" /number=14	/gene="act" /product="amylose extender starch-branching enzyme" /poin(<61190,277387,536>668) /gene="act" /codon_start=2 /product="amylose extender starch-branching enzyme" /protein_id="AAP03849.1" /bratein_id="AAP03849.1" /db_xref="GI:30014018"	/organism="Zea mays subsp. mays" /mol_type="genomic_DNA" /cultivar="CIL87-2" /sub_species="mays" /db_xref="taxon:4578" <1 713 /gene="sel" join(<61. 190,277. 387,536>668)	Direct Sub Submitted University	Zea mays subsp. mays Eukaryota; Subsp. mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 713) Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,B.S. Genetic diversity and selection in the maize starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002) 22247734 12244216 2 (bases 1 to 713) Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S. IV.	bsp. ching	481 ATATTTGTTATATCATTCCTTCTTATCTAAAGTCA
DS DS NISM NISM NCE ORS	RESULT 14 AY235698 AY235698 AY235698 DEFINITION Zea mays subsp. mays cultivar CMIZ554 amylose extender starch-branching enzyme (ael) gene, exons 12, 13, and 14 and AY235698 ACCESSION AY235698	OY 1943 ATTITGGATTTGCTACTGATGTTGATGCTGGTAGTTTACTTGATGCTGGTCAACGATCTAA 2002	Db 481 ATATTGTTATATACATTCCTTCTTCTAGATCAAGTCA	317 AGGAATATAAGTTTGATGATGATGATGATGATGATGATGA	1523 197 1583 257	Query Match Best Local Similarity 65.1%; Pred. No. 1.7e-40; Matches 461; Conservative 0; Mismatches 192; Indels 55; Gaps 4; Matches 461; Conservative 0; Mismatches 192; Indels 55; Gaps 4; 1343 TICAGTIGATIGATIGATIGATIGATIGATIGATIGATIGATI

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TGATGCTGGTAAATGATCTAA 623
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ATGTAAGTG 671
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Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA Location/Qualifiers
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Whitt, S.R., Wilson, L.M.,
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GCTATGCATCATAACATGTATCATGATCAGGACTTGTGCTACGGAGTCTTAGATAGTTCC
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                                                                                                                                                            AAGAATATAAGTTTGATGGATTTCGATTTGATGGGGTGACCTCCATGATGTATACTCACC 1702
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ilarity 65.1%;
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/gene="ae1"
/number=14
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/number=12
277. .387
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LRFLLSNARWWLEEYKFDGFRFDGVTSMYYTHHGLQVTFTGNFNEYFGFATDVDAVVY
LMLVNDLIHGLYPEAVTIGEDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sub_species="mays"
/db_xref="taxon:4578"
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/mol_type="genomic DNA"
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/protein_id="AAP03850.1"
/db_xref="GI:30014020"
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Pred. No. 1.7e-40;
0; Mismatches 192;
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Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 713)
Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
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Whitt, S.R., Wilson, L.M.,
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277. .387
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join(<61. .190,277. .387,536. .>668)
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The invention relates to a novel enzyme of starch biosynthetic pathway in a cereal plant, where the enzyme is selected from starch branching enzyme (SBE) I , SBE II, starch soluble synthase (SSS) I, and debranching enzyme
                                                                                                    New isolated cereal plant enzyme genes used for, earntisense sequences of granule bound synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Starch branching enzyme II (SBE II)
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Aat467260 Rice gene
Aad472110 Rice gene
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Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS; starch branching enzyme; starch soluble synthase; debranching enzyme; endosperm; wheat; barley; granule-bound synthase; glutenin; starch; grain softness protein I; bacterial isoamylase; glycogen synthase; wSBE I-D4 gene; ss.
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dd	6748 TTTACTGGGAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGATGCGGTAGTTTAC 6807	ਰਹ	4941 TATTCACACAATCCATTTTTTTCTGTATACACNTCTTCACCCATTTGGAGCTATTACATC 5000
Qу	1981 TIGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTATCCATTGGTGAA 2040	Qy db	180 CTAATGOTTCATGCACATAAAATATTTGGATATAAATCCTTTATTAGATATATAT
QQ VQ	2041 GATGTAAGTG 2050 6868 GATGTAAGTG 6877	Qy Db	240 TACACTTAGTATTCTGAAAAAGATCATTTTATTGTTGTTGTTGCTTGCTAGGTACCA 296
RESULT 2 AAH78338		dg VQ	297 TGTTACTAATTTTTTTGCACCAAGTAGCCGTTTTGGAACTCCAGAGGACTTAAAATCCTT 356
8×5	AAH78338 standard; cDNA; 11475 BP. AAH78338;	. Q	GATCGATAGAGCACATGAGCTTGGTTTGCTTGTTCTTATGGATATTGTTCATAGGTAAIT 4
{	26-NOV-2001 (first entry)	Ş B	GATCGATAGAGCACATGAGCTTGGTTTGCTTGTTCTTATGGATATTGTTCGTAGGGA
XEX	Nucleotide sequence of a starch branching enzyme designated F2.	g dy	417 AGTCCAATTTAACTTTTAACTGTTTATCTGGTATTCTAAAGGAAAATTCAGGC 4/6
22	Wheat; starch branching enzyme; BEIIb; SBE; transgenic plant; starch biosynthetic pathway; amylopectin; F2; amylose; ss.	Ş Ş	AATTATGATACATTGTCAAAAGCTAAGAGTGGCGAAAGTGAAATGTCAAAATCTAGAGTG
\$ S \$	Aegilops tauschii.	дb	5301 AATTATGATACATTGTCAAAAAGCTAAGAGTGGCGAAAAGTGAAATGTCAAAATCTAGAGTG 5360
ΧRX	WO200162934-A1.	γŞ	537 GCATAAGGAAAATTGGCAAAAACTAGAGTGGCAAAAATAAAATTTTTCCCATCCTAAAATGG 596
X B X	30-AUG-2001.	₽	5361 GCATAAGGAAAATTGGCAAAAACTAGAGTGGCAAAAATTAAAATTTTCCCATCCTAAATGG 5420
Z X F	21-FEB-2001; 2001WO-AU000175. 21-FEB-2000; 2000AU-00005742.	당 &	597 CAGGGCCCTATCGCCGAATATTTTTCCATTCTATATAATTGTGCTACGTGACTTCTTTTT 656
PA PA PA	(CSIR) COMMONWEALTH SCI & IND RES ORG. (GOOD-) GOODMAN FIELDER LTD. (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.	QQ dd	657 TCTCAGATGTATTAAACCAGTTGGACATGAAATGTATTTTGGTACATGTAGTAACTGACA 716
\$ E \$	Morell M, Rahman S;	Ωγ	717 GTTCCATAGAATATCGTTTTGTAATGGCAACAATTTGATGCCATAGATGTGGATTGAG 776
X & X	WPI; 2001-570635/64.	מם	5541 GTTCCATAGAATATCGTTTTTGTAATGGCAACACAATTTGATGCCATAGATGTGGATTGAG 5600
rg p p ?	Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. wheat and barley.	D Qy	777 AAGTTCAGATGCTATCAATAGAATTAATCAACTGGCCATGTACTCGTGGCACTACATATA 836
	rch branching enzyme of Aeg	р Q	837 GTTTGCAAGTTGGAAAACTGACAGCAATACCTCACTGATAAGTGGCCAGGCCCCACTTGC 896
	tauschii, designated F2. A. tauschii is likely to be the ancestral D genome donor of wheat. Probes isolated from the present sequence were used to identify type II starch branching enzymes (SBEs) in wheat, especially BEIIb. The BEIIb nucleic acids may be used to genetically	D Q	897 CAGCTTCATACTAGATGTTACTTCCCTGTTGAATTCATTTGAACATATTACTTAAAGTTC 956
	arch biosynthetic pathw	Qy Db	957 TICATITGICCTAAGICAAACITCITTAAGITTGACCAAGICTATIGGAAAAATATATCAA 1016
Que Que	98.8%; Score 2025; DB 5; Length 11475; 99.8%; Pred. No. 0;	Qy Db	1017 CATCTACAACACCAAATTACTTTGATCAGATTAACAATTTTTATTTA
D VQ	PARTYCATARTCCTAATTTAGGGATGAGGTGTTGCCAAGAATTAAAAGGCTTT	р Qy	1077 ATCTTTGATGTTGTAGATATCAGCACATTTTTCTATAGACTTGGTCAAATATAGAGAAGT 1136
Å Å	GGATACAATGCAGTGCAGATAATGGCAATCCAGGAGCATTCATACTATGCAAGCTTTGGG 120	ଟ ପ୍ର	1137 TIGACTTAGGACAAATCTAGAACTTCAATCAATTTGGATCAGAGGGAACATCAAATAATA 1196 5961 TIGACTTAGGACAAATCTAGAACTTCAATCAATTTGGATCAGAGGGAACATCAAATAATA 6020
5 B	4881 GATACAATGCAGTGCAGATAATGGCAATCCAGGAGCATTCATACTATGCAAGCTTTTGGG 4940 121 TATTCACACACATCCATTTTTTTCTGTATACAC-TCTTCACCCATTTGGAGCTATTACATC 179	Qy	1197 TAGATAGATGTCAACACTTCAACAAAAAAATCAGACCTTGTCACCATATATGCATCAGAC 1256

707447071	X A X E	B 8	g &	g &	8 8	A A	QQ VQ	ρ δ	g Q	P Q	g Qy	Å Å	망양	g &	40
27-MAR-2000 (first entry) Maize amylose-extender (Ae) gene encoding starch branching enzyme. Maize amylose-extender gene; Ae gene; maize; corn; promoter; expression control element; endosperm; transgenic plant; ss. Zea mays.	03.93; Braildard; C	2037 TGAAGATGTAAGTG 2050 	1977 TTACTTGATGCTGATCAACGATCTAATTCATGGACTTTATCCTGATGCTGTATCCATTGG 2036	1917 GACATTTACTGGGAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGATGCGGTAGT 1976 	1857 ATGGAAGATTGGAAGTGATTATTATTTATTTCTTTCTAAGTTTGTTCTTGTTCTAGAT 1916 	1797 TGTGCTACGGAGTCTTAGATAGTTCCCTAGTATGCTTGTACAATTTTACCTGATGAGATC 1856	1737 AACITITITAGGGCACTGAAACAATTGCTATGCATCATAACATGTATCATGATCAGGACT 1796 	1677 GGTGACCTCCATGATGTATACTCACCATGGATTACAAGTAAGT	1617 ACTGTCAAACGCGAGATGGTGGCTTGAAGAATATAAGTTTGATGGATTTCGATTTGATGG 1676	6 H	1497 AACTATGGGAGTTGGGAAGTATGTAGCTCTGACTTCTGTCACCATATTTGGCTAACTGTT 1556	437 ACACATTACTTCCACGGTGGTCCACGCGGCCATCATTGGATGTGGGATTCTCGTCTATTC 149	1377 CCCTGCAGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGAT 1436 	1317 CTTCTACTTGGTTTGATTCTATTTCAGTTGCATTGCTTCATCAATGATTTTGTGTA 1376	1257 CATCTGTTTGCTTTAGCCACTTGCTTTCATATTTATGTGTTTGTACCTAATCTACTTTTC 1316
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FT intron FT exon FT intron FT intron	FT exon	FT intron FT exon	FT exon		FT intron	FT exon		exon CDS	FT GC_signal FT TATA_signal FT	misc	FT GC_signal	GC E	FT misc_signal	misc_s	FH Key FT misc_signal FT FT FT repeat unit

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                                                                                                                                                                                                                                                                                                                                                                                                                            New gene regulatory sequences from plants used to provide resistance microbial path pathogens.
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12-JUN-1998;
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   12921
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                                                                                           1463 CGGCCATCATTGGATGTGGGATTCTCGTCTATTCAACTATGGGAGTTGGGAAGTATGTAG
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                                               AGGAATATAAGTTTGATGGTTTTGATGGTGTGACCTCCATGATGTACACTCATC
                                                                    AAGAATATAAGTTTGATGGATTTCGATTTGATGGGGTGACCTCCATGATGTATACTCACC
                                                                                                                                                                CTCTGACTTCTGTCACCATATTTGGCTAACTGTTCCTGTTAATCTGTTCTTACACATGTT
                                                                                                                                                                                         TGGCCATCACTGGATGTGGGATTCTCGCCTATTTAACTATGGGAACTGGGAAGTACG---G
   ACGGATTACAAGTAATTTAAGCTTTATGCCTGTTAGTTTATCT
                       ATGGATTACAAGTAAGTCATCAAGTGGTTTCAGTAACTTTTTTAGGGCACTGAAACAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim K;
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98US-0089050P.
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Query Match 11.8
Best Local Similarity 63.1
Matches 463; Conservative
                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding wheat starch branching enzyme IIb, useful altering the amylose and amylopectin content of cereal plants, \boldsymbol{e}. and barley.
                                                                                                                                                      The present sequence represents a partial genomic sequence of a wheat starch branching enzyme, designated BEIIb. BEIIb is a type II starch branching enzyme (SBE). The BEIIb nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH78343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH78343 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-2001
                                                                                              Sequence
                                                                                                                                                                                                                                                                                                    Claim 6; Page 95-98; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morell M,
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(GOOD-) GOODMAN FIELDER LTD.
(LIMA-) GRP LIMAGRAIN PACIFIC PTY I
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biosynthetic pathway;
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                                                                                              2134 A; 1788 C;
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               Score 241.2; DB 5;
Pred. No. 9.6e-46;
0; Mismatches 223;
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starch
                                                                                                                                                                                                                           Nucleotide sequence
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21-FEB-2001; 2001WO-AU000175
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                                                                                                                        Triticum
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                                                                                                                                                            starch branching enzyme; BEIIa; biosynthetic pathway; amylopecti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTACTTGATGCTGATGATGATCTAATTCATGGGTTTTATCCTGAAGCCGTAACTATCGG
                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                           of wheat starch branching enzyme 9 (BEIIa)
                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---aacctaaattactttttttttgaattgctgcgctctattttaggt
                                                                                                                                                                 amylopectin;
                                                                                                                                                                                                                                                                                                                                                     ₽P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -TAGTATCAATTTTTATTTGAGCTTGA-----
                                                                                                                                                                 BEIIb; SBE;
in; amylose;
                                                                                                                                                                                      SBE;
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AAX34650/c
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Query Match
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Matches 242
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       Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS; starch branching enzyme; starch soluble synthase; debranching enzyme; endosperm; wheat; barley; granule-bound synthase; glutenin; starch; grain softness protein I; bacterial isoamylase; glycogen synthase; wSBE I-D4 gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2726 BP; 726 A; 564 C; 701 G; 735 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. wheat
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                                                                                                                                                      17-OCT-2003
05-JUL-1999
                                                                                                                                                                                                                                              AAX34650 standard; DNA; 11473
                                                                                                                  Starch branching enzyme II (SBE II) gene sequence.
                                                                                                                                                                                                          AAX34650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1383 AGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1228 TACTTCCACGGTGGTCCACGTGGCCATCATTGGATGTGGGATTCTCGTCTATTCAACTAT 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                       CTCCATGATGTATACTCACCATGGATTACAAGTAA 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGAGTTGGGAAGTATGTAGCTCTGACTTCTGTCACCATATTTGGCTAACTGTTCCTGTT
                                                                                                                                                                                                                                                                                                                                      CTCCATGATGTATACTCACCATGGATTACAAATGA 1414
                                                                                                                                                                                                                                                                                                                                                                                                          AAACGCGAGATGGTGGCTTGAAGAATATAAGTTTGATGGATTTCGATTTGATGGGGTGAC
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                                                                                                                                                      (first entry)
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RESULT 7 AAH78338/c ID AAH783

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Best Local Similarity 64.6%;
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel enzyme of starch biosynthetic pathway in a cereal plant, where the enzyme is selected from starch branching enzyme (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of rice or maize. The methods and products can be used for targeting expression specifically to the endosperm of the seeds of cereal plants such as wheat or barley. They can be used for the expression of e.g. antisense sequences of granule-bound synthase (GBSS), SBE II, low mol. wt. glutenin, grain softness protein I, bacterial isoamylase, bacterial glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be used for modifying the characteristics of starch produced by a plant. The present sequence represents the SBE II gene sequence. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated cereal plant enzyme genes used for, e.g. expression antisense sequences of granule bound synthase.
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20-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11473 BP; 3096 A; 2263 C; 2423 G;
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(AUSU )
(GOOD-)
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GOODMAN FIELDER LTD.
GRP LIMAGRAIN PACIFIC I
                                                                                                                                                                                                                                                                                                                        GTCAAACTTCTCTATATTTGACCAAGTCTATAGAAAAATGTGCTGATATCTACAACATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGITACTTCCCTGITGAATTCATTTGAACATATTACTTAAAGTTCTTCATITGTCCTAA
                              ATCTAGAACTTCAATCAATTTGGATCAGAGGGAACATCAAATAATATAGAT 1201
                                                                                                                                                         AGATATCAGCACATTTTTCTATAGACTTGGTCAAATATAGAGAAGTTTGACTTAGGACAA
                                                                                                                                                                                                                                                           AATTACTTTGATCAGATTAACAATTTTTATTTTATTATTAGCACATCTTTGATGTTGT
                                                                                                                                                                                                                                                                                                                                                            GTCAAACTTCTTTAAGTTTGACCAAGTCTATTGGAAAATATATCAACATCTACAACACCCA 1030
                                                                                                                                                                                                                                                                                                                                                                                                                               AAGATGTGCTAATATAATAAAATAAAATTGTTAATCTGATCAAAGTAATTTGGTGTTGT
ATGAAGAACTTTAAGTAATATGTTCAAATGAATTCAACAGGGAAGTAACAT 5738
                                                                                                       AGATGTTGATATATTTTCCAATAGACTTGGTCAAACTTAAAGAAGTTTGACTTAGGACAA
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98AU-00002509
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Pred. No. 5.2e-19;
0; Mismatches 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3691 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 11473;
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Matches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a wheat starch branching enzyme of Aegilops tauschii, designated F2. A. tauschii is likely to be the ancestral D genome donor of wheat. Probes isolated from the present sequence were used to identify type II starch branching enzymes (SBEs) in wheat, especially BSIID. The BEIID nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to var levels of amylopectin and/or amylose produced in the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wheat;
starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. wheat
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11475
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                                              ADC08218
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biosynthetic pat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMONWEALTH SCI & IND RES GOODMAN FIELDER LTD.
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRP LIMAGRAIN PACIFIC
                                                                                                                                                                                                                                                                   ATCTAGAACTTCAATTTGGATCAGAGGGAACATCAAATAATATAGAT 1201
                                                                                                                                                                                  AGATATCAGCACATTTTTCTATAGACTTGGTCAAATATAGAGAAGTTTGGCTTAGGACAA 1150
                                                                                                                                                                                                                                       AATTACTTTGATCAGATTAACAATTTTTATTTATTATATTAGCACATCTTTGATGTTGT
                                                                                                                                                                                                                                                                                                                      ATCTATATTAGATGTTCCCTCTGATCCAAATTGATTGAAGTTCTAGATTTGTCCTAA
                                                                                                                                                                                                                                                                                                                                                ATGTTACTTCCCTGTTGAATTCATTTGAACATATTACTTAAAGTTCTTCATTTGTCCTAA
                                              standard;
                                                                                                                                                                                                                  <u>AAGATGTGCTAATATAATAAAATAAAAATTGTTÄATCTGATCAAAGTAATTTGGTGTTGT</u>
                                                                                                            <u> ATGAAGAACTTTAAGTAATATGTTCAAATGAATTCAACAGGGAAGTAACAT</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rahman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 3093 A; 2259 C; 2423 G; 3689 T; 0 U; 11 Other;
                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                      64.6%;
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                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                         Score 126.2; DB 5;
Pred. No. 5.2e-19;
0; Mismatches 103;
                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIY ALD
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ylopectin; F2; amylose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             branching
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 11475;
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Zhu T, Cheng W, Briggs S,
Glazebrook J, Katagiri F,
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26-SEP-2001; 2001US-0325277P.
20-DEC-2001; 2001US-0342327P.
                                                                                                                                                                                                                                                                                                                                             Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                             gene;
                                                                                                                                                                                                                                                                                                                                                                    plant biotechnology; carbohydrate synthesis; carbohydrate metabolism; carbohydrate degradation; carbohydrate; plant grain; grain filling; corn; tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet; wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
                                                                                                                                                                                                                                                                                                                                                                                                             Rice
                                                                                                                                                                                                                                                                                               21-JUN-2002; 2002WO-IB002450
                                                                                                                                                                                                                                                                                                              03-JAN-2003
                                                                                                                                                                                                                                                                                                                               WO2003000905-A2
                                                                                                                                                                                                                                              (SYGN )
                                                                                                                                                                                               2003-229341/22.
DB; ADC08219.
                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence
                                                                                                                                                                                                                                                                                                                                                            ds; plant
                                                                                                                                                                                                                                               SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                                                                             Seq
                                                                                                                                                                                                                                                                                                                                                                                                             ID523
                                                                                                                                                                                                                     Cooper B, Goff SA,
Kreps J, Provart N,
                                                                                                                                                                                                                                                                                                                                                                                                             related
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                                                                                                                                                                                                                                                                                                                                                                                                             grain
                                                                                                                                                                                                                                                                                                                                                                                                             filling
                                                                                                                                                                                                                       Moughamer
Ricke D;
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in the plant grain useful in generating nutritional properties. New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved

Claim 35; SEQ ID NO 523; 130pp; English

This invention, in the area of plant biotechnology, relates to novel polymucleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence encoding a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at

Sequence 2304 BP; 610 A; 457 C; 620 G; 617 T; 0 U; 0 Other;

Similarity

6.0%;

DB 9; 12;

Length

2304; 0;

Indels

Gaps

0

δÃ 片 δ 밁 Ś 뮍 Query Match
Best Local Sim
Matches 130; 1969 1354 1909 TTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGAT GCCATTGGTGAAGATGTCAGCG TCCATTGGTGAAGATGTAAGTG Conservative <u>.</u> Score 122.8; DB Pred. No. 2e-18; 0; Mismatches 1495 2050 2028 1473 1413 1968

RESULT 9 ADA71289 ID ADA71289

18-15-2002 ADC08218;

standard; DNA; ВP

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RESULT 10
AAV05639
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                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 130; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to pacterial, fingal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chang H,
Katagiri
      25-MAR-2003
01-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; SEQ ID NO 4612; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant; bacterial infection;
gene; ds.
                                                                                                                                                                                                                                                                                                                                                  Sequence 2655 BP; 714 A; 529 C; 680 G; 732 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice gene,
                                              AAV05639;
                                                                       AAV05639 standard; cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-2001; 2001WO-IB001105
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                                                                                                                                                                                                       GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA 2028
                                                                                                                                                              TCCATTGGTGAAGATGTAAGTG
                                                                                                                                                                                                                                              TTACAGGTGGCATTTACTGGCAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGAT
                                                                                                                                                                                                                                                              TTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTTGGATTTGCTACTGATGTTGAT 1968
                                                                                                                                        GCCATTGGTGAAGATGTCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID 4612
                                                                                                                                                                                                                                                                                                                                                                              the invention.
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     (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                            6.0%;
91.5%;
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s, Tao
                                                                       to mRNA;
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                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                            Score 122.8; DB 7
Pred. No. 2.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glazebrook J, Goff SA, Whitham S, Xie Z, Zhu
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RESULT 11
ADC07807
ID ADC07
XX ADC07
XX ADC07
XX ADC07
XX 18-DE
XX 18-DE
XX Plant
XW Carbo
KW Carbo
KW Carbo
KW Carbo
KW Carbo
KW Carbo
KW Grenet
KW Grenet
KW Grenet

ADC07807 standard; DNA; 2307

Rice DNA sequence Seq ID73 related to grain filling.

(first entry)

plant biotechnology; carbohydrate synthesis; carbohydrate metabolism; carbohydrate degradation; carbohydrate; plant grain; grain filling; corn; comato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet; wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain; gene: dg: plant

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Best Local Sim.
Matches 130;
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                                                                                                                                                                 Sequence 3015 BP; 796 A; 606 C; 819 G; 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cbs
                                                                                                                                                                                      The present sequence encodes the rice type IV starch branching enzyme, which has the ability to synthesise amylopectin. The quality of starch improved by the use of the protein. (Updated on 25-MAR-2003 to correct field.)
                                                                                                                                                                                                                                                              quality starch.
                                                                                                                                                                                                                                                                      Rice starch branching enzyme gene -
                                                                                                                                                                                                                                                                                                       WPI; 1998-133625/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice
                                                                                                                                                                                                                                       Claim 4; Page 5-8; 13pp; Japanese
                                                                                                                                                                                                                                                                                             P-PSDB; AAW41763.
                                                                                                                                                                                                                                                                                                                           (MITS-) MITSUI
                                                                                                                                                                                                                                                                                                                                                          24-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type IV
                                                                                                                                    Similarity
              TCCATTGGTGAAGATGTAAGTG 2050
                                                                                                     TTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGAT
GCCATTGGTGAAGATGTCAGCG 1767
                                        GCAGTAGTTTACTTGATGCTGGTGAACGATCTAATTCATGGGCTTTATCCTGAGGCTGTA
                                                           GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA
                                                                                 TTACAGGTGGCATTTACTGGCCAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGAT
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                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            starch branching enzyme; amylopectin synthesis;
                                                                                                                                                                                                                                                                                                                           GYOSAI SHOKUBUTSU TOATSU CHEM INC.
                                                                                                                                                                                                                                                                                                                                                           96JP-00162983
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288. .2651
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129. .287
                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= c
/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                         6.0%; Score 122.8; DB 2;
91.5%; Pred. No. 2.2e-18;
tive 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                           "type_IV_starch_branching_enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme
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                                                                                                                                                                                                                                                                         synthesises amylopectin to yield high
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                                                                                                                                             Length 3015;
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AAT69737
ID AAT69737
ID AAT69737
XX AAT69
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Best Local Sim.
Matches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence encoding a rice protein of the invention. Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved nutritional properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhu T, Cheng W, Briggs
Glazebrook J, Katagiri I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-2001; 2001US-0300112P.
26-SEP-2001; 2001US-0325277P.
20-DEC-2001; 2001US-0342327P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUN-2002; 2002WO-IB002450
Starch branching enzyme IIb; SBEIIb; corn; maize; antisense; amylopectin;
                                                     Corn starch
                                                                                                              10-SEP-1997
                                                                                                                                                                       AAT69737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 73; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          ATCCTGATGCTGTATCCATTGGTGAAGATGTAAGTG 2050
                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGTATACTCATCATGGTTTACAGCATTTACTGGCAACTATGGCGAATATTTTGGATTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2307 BP; 608 A; 465 C; 620 G; 614 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                             ATCCTGAGGCTGTAGCCATTGGTGAAGATGTCAGCG 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTACTGATGTTGATGCAGTAGTTTACTTGATGCTGGAACGATCTAATTCATGGGCTTT
                                                  branching enzyme
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                                                                                                              (first entry)
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                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.38;
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Kreps J,
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0; Mismatches 23
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                                                     IIb gene fragment in pBE96
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, Provart N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
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Ricke D;
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AAT69736;
ID AAT69736;
XX AAT69736;
AC AAT69736;
XX DE Corn starc
XX DE Corn starch brack
XX Starch brack
XX Starch brack
XX Starch brack
XX W Starch brack
XX DE COUN-19;
XX Zea mays.
PN WO9722703
XX PD 26-JUN-19;
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Best Local S
Matches 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A cDNA insert (AAT69737) in plasmid pBE96 comprises a 2.09 kb fragment of corn starch branching enzyme IIb (SBEIIb) cDNA (see also AAT69729), starting at the initiating ATG codon of the coding region and terminating 312 bp 5' of the translation termination codon. It was obtd. by site-specific mutagenesis of the SBEIIb gene in plasmid pBE240 to generate an NcoI site at the ATG start site, and EcoRI digestion of the mutagenised plasmid. The 2.09 kb fragment was inserted, in sense orientation, between the zein promoter and 3' regions in vector pML103 to produce pBE96. Cosuppression and antisense techniques can be used to inhibit SBEIIb in transgenic plants and thereby alter starch properties
                                                                                                            Starch branching enzyme IIb; transgenic plant; pBE45; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2087 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic corn in which grain derived starch fine structure controlled - specifically branch chain distribution of amylop useful in preparation of thickened foodstuff.
                                                                                                                                                             Corn starch branching enzyme IIb gene fragment in
                                                                                                                                                                                             10-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Page 56-57; 92pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hubbard NL,
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                                                 WO9722703-A2
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131; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTCATGCGTCAAGTAATACTCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACAT 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACAT 1442
                                                                                                                                                                                                                                                              standard; DNA;
                                                                                                                                                                                                                                                                                                                                            GGGAACTGGGAAGTTTTAAGATTTCTTCTCTCCAATGCTAGATGG
                                                                                                                                                                                                                                                                                                                                                                          TACTTTCACAGTGGTCCACGTGGCCATCACTGGATGTGGGGATTCTCGCCTATTTAACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                           TACTTCCACGGTGGTCCACGGGGCCATCATTGGATGTGGGATTCTCGTCTATTCAACTAT 1502
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                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          565 A; 396 C; 553 G;
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K
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                                                                                                                                                                                                                                                               ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 110.6; DB 2
Pred. No. 1.3e-15;
                                                                                                                                SBEIIb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                  corn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          573 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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RESULT 14
AAV70961
IID AAV70
XX AV70
XX AV70
XX AV70
XX DNA e
XX NON-9
KW Starco
KW non-e
KW non-e
KW non-e
XX NO984
XX 15-00
XX 03-Ai
PF 03-Ai
XX X
PR 04-Ai
PR (EXSI
PA (EXSI
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Best Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A 2.16 kb cDNA insert (AAT69736) in plasmid pBE45 comprises the entire 5' untranslated region as well as 2.08 kb of the coding region of corn starch branching enzyme IIb (SBEIIb) cDNA (see also AAT69729). It was generated by EcoRI digestion of plasmid pBE240 and was inserted into vector pMLD103 in antisense orientation with respect to a maize 27 kba zein promoter and a 10 kba zein gene 3' sequence. Transgenic corn plants expressing the near full-length SBEIIb antisense transcript demonstrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic corn in which grain derived starch fine structure is controlled - specifically branch chain distribution of amylopectin, useful in preparation of thickened foodstuff.
                                                                                                                                                                                                                     Non-glycogen-like polysaccharide production; fermentation; starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthe non-starch branching gene; amylopectin; amylose; plant-like starch; maize branching enzyme II; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2165 BP; 593 A; 580 C; 416 G; 576 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 55-56; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-341694/31.
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                                                                                                                                                                                                                                                                                                                                                           AAV70961;
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                                                                          04-APR-1997;
                                                                                                                                  15-OCT-1998
                                                                                                                                                                WC9844780-A1
                                                                                                                                                                                                                                                                                                DNA encoding
                                                                                                                                                                                                                                                                                                                             23-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                       AAV70961 standard; DNA;
                                                                                                     03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unique starch branching phenotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACAT 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGAGTTGGGAAGTATGTAGCTCTGACTTCTGTCACCATATTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTCATGCGTCAAGTAATACTCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGAACTGGGAAGTTTTAAGATTTCTTCTCCCAATGCTAGATGG
              Keeling PL
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                                                                                                                                                                                                                                                                                                                             (first entry)
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                                             GENETICS LLC
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                                                                                                      98WO-US006660.
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                                                                                                                                                                                                                                                                                                branching enzyme II.
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79.4%;
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Pred. No. 1.3e-15;
0; Mismatches 34;
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                                                                                                                                                                                                                                                         synthesis;
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RESULT 15
AAT69729
ID AAT69729
XX AAT69
XX AAT69
XX Plasm
XX Starc
KW Starc
KW Crans
XX Zea m
XX CDS
FT CDS
FT CDS
FT CDS
FT 12-DE
XX (DUPC
XX (DUP
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes a method for the production of non-glycogen-like polysaccharides in a host. The method comprises transforming a host, suitable for fermentation, with genes encoding starch- or glycogen-synthesis enzymes, and fermenting the transformants. The specification also describes hosts transformed with a gene active in glycogen synthesis and at least one non-starch branching gene, involved in production of amylopectin or amylose in its original host. The method is used to produce plant-like starches by fermentation and non-food applications of these starches are useful for all food and non-food applications of starch. The present sequence is used in the course of the invention
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transformed with genes for enzymes involved in starch or glycogen
synthesis allows fermentative production of starches with engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2640 BP; 715 A; 510 C; 686 G; 729 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT69729 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT69729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pBE240 insert encoding corn
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                                                                                                                                                                                                        20-DEC-1995;
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DB; AAW70895.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGAACTGGGAAGTTTTAAGATTTCTTCTCTCCAATGCTAGATGG
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                                                                                                                                                                                                        95US-0009113P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 79. .2478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme IIb; ; pBE240; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA; 2665
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Pred. No. 1.4e-15;
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WPI; 1997-341694/31. P-PSDB; AAW19212.

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Broglie KE

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Search completed: April 10, 2004, 04:00:06 
Job time : 808.094 secs
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                                                                                                                                                                                                                                                                                                                                 Transgenic corn in which grain derived starch fine structure is controlled - specifically branch chain distribution of amylopectin, useful in preparation of thickened foodstuff.
                                                                                                                                                                                                                                                                                                    Sequence 2665 BP; 700 A; 525 C; 705 G; 735 T; 0 U; 0 Other;
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2. /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4. /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6. /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Patent No. 6570066

GENERAL INFORMATION:
APPLICANT: Willmitzer, et al.
APPLICANT: Willmitzer, et al.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZY
TITLE OF INVENTION: CONCENTRATION AND COMPOSITION IN
FILE REFERENCE: 514413-3515.1

CURRENT APPLICATION NUMBER: US/09/609,040

CURRENT FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: PCT/EP92/00302

PRIOR FILING DATE: 1992-02-11

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.0

LENGTH: 2853
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CAGANISM: Triticum a
FEATURE:
NAME/KEY: CDS
LOCATION: (313)...(24
OTHER INFORMATION: B
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Matches 244;
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                            AAACGCGAGATGGTGGCTTGAAGAATATAAGTTTGATGGÄTTTCGATTTGATGGGGTGAC
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Pred. No. 1.9e-28;
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PATENT NO. 6639126
GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified
FILE REFERENCE: 35718/206348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Apprair

Sequence 
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Best Local Similarity
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CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atent No. 6376749
GENERAL INFORMATION:
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LOCATION: (0)...(0)
OTHER INFORMATION: SBEIIA
OTHER INFORMATION: Genbank Accession No. 6639126 U65948
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ORGANISM: Zea mays
FEATURE:
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LOCATION: (2)...(2446)
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APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
                                                                                                                                                        STREET: lvv,
CITY: Wilmington
STATE: Delaware
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC comparible
OPERATING SYSTEM: Microsoft Windows 95
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Broglie, Karen E. APPLICANT: Klein, Theodore M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                  ADDRESSEE:
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1007 Market Street
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SEQUENCE CHARACTERISTICS:
LENGTH: 2087 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOROLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Sim: Matches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Broglie Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el S!
TITLE OF INVENTION: Expression of S!
TITLE OF INVENTION: Expression of S!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Majarian, William R. REGISTRATION NUMBER: 41.173
REFERENCE/DOCKET NUMBER: BB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Form Compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 09/0
FILING DATE: JUNE 10, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Version 7.0A CURRENT APPLICATION DATA:
         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1007 Mari
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                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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5. 6376749
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31; Conservative
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1007 Market Street
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79.48;
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Pred. No. 1.4e-19;
0; Mismatches 34
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Patent No. 6376749
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                 CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,
PILING DATE: JUNE 10, 1998
ATTORNEY/ACENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Broglie, Karen b.
APPLICANT: Klein, Theodore M.
APPLICANT: Klein, Theodore M.
APPLICANT: Lightner, Jonathan E.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-
FELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
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REFERENCE/DOCKET NUMBER: BB-1066-A
                                                                                                                                                                                                                      APPLICATION NUMBER:
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CITY: Wilmington
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TYPE: nucleic acid
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1007 Market Street
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TACTICCACGGTGGTCCACGCGGCCATCATTGGATGTGGGATTCTCGTCTATTCAACTAT 1502

TACTTTCACAGTGGTCCACGTGGCCATCACTGGATGTGGGATTCTCGCCTATTTAACTAT

1358

GGGAGTTGGGAAGTATGTAGCTCTGACTTCTGTCACATATTTG

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; NAME/KEY:
; LOCATION:
US-09-257-894-1
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; Sequence 11, Application US/09731166
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SEQ ID NO 11
LENGTH: 2720
                                                                         Query Match 5.4%;
Best Local Similarity 79.4%;
Matches 131; Conservative
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Best Local Similarity 79.4%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6639126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified Polysaccarides
FILE REFERENCE: 35718/206348
CURRENT APPLICATION NUMBER: US/09/731,166
CURRENT FILING DATE: 2000-12-06
CURRENT FILING DATE: 2000-12-06
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/169,993
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (101)...(2500)
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                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2665 base pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: sing
                      1383 AGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACAT 1442
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AGTCATGCGTCAAGTAATACTCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACAT 1297
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Pred. No. 1.6e-19;
0; Mismatches 34
                                                                         Score 110.6; DB 4
Pred. No. 1.6e-19;
0; Mismatches 34
                                                                                                                                                                                                                       6639126 AF072725
                                                                                                                   DB 4;
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RESULT 7
US-08-941-445A-14
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                                                                                                                                                                                                   Query Match
Best Local S
                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (303) 499-80 TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2725 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION
7272 AGG_8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Keeling, Peter
APPLICANT: Guan, Hamping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOPOTORY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ECULE TYPE: mkw
                                                                                          1443
                                                                                                                         1228
1348
                                                                                                                                                     1383 AGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACAT 1442
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6107060
                                                                                                                                                                                                   Similarity
                          GGGAGTTGGGAAGTATGTAGCTCTGACTTCTGTCACCATATTTGG 1547
                                                                                                                         AGTCATGCGTCAAGTAATACTCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACAT
GGGAACTGGGAAGTTTTAAGATTTCTTCTCTCCAATGCTAGATGG 1392
                                                            TACTTTCACAGTGGTCCACGTGGCCATCACTGGATGTGGGATTCTCGCCTATTTAACTAT 1347
                                                                                        TACTTCCACGGTGGTCCACGCGGCCATCATTGGATGTGGGATTCTCGTCTATTCAACTAT
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                                                                                                                                                                                      Conservative
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265..2487
                                                                                                                                                                                                                                                                                                                                                           sig_peptide
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30-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
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Pred. No. 1.6e-19;
                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                  Length 2725;
                                                                                                                                                                                      Indels
                                                                                                                                                                                     0;
                                                                                                                                                                                   Gaps
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RESULT 9 US-09-658-499-3

Sequence 3,

Application US/09658499

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APPLICANT: EK, BO
APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, HAKAN
APPLICANT: LARSSON, HAKAN
APPLICANT: LARSSON, HAKAN
APPLICANT: RASK, LATS
ITILE OF INVENTION: STARCH BRANCHING ENZYME II
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER APPLICATION NUMBER: SE 9504270-7
EARLIER FILING DATE: 1995-01-10-20
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
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, NAME/KEY: misc feature
; LOCATION: (1148)..(1150)
; OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa
US-09-087-277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-087-277-3
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                                                                                                                                                                                                                                                                                                Query Match

Best Local Similarity 78.9

Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (890)..(892)
OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser,
OTHER_INFORMATION: or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (424)..(1150)
OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n
OTHER INFORMATION: C, G or T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism:beII gene fragment
OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
OTHER INFORMATION: (potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (422)..(424)
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LOCATION: (2)..(1393)
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                                                                                                                                                                                                                                       1909 TTCTAGATGACATTTACTGGGGAACTATGGCGAATATTTTGGATTTTGCTACTGATGTTGAT
                                              2029 TCCATTGGTGAAGATGTAAGTG 2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION: Amino acid 141 is Xaa wherein Xaa =
                                                                                                794
                                                                                                                                                                                                734 TTATCGGTGGGATTCACTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGAT
                                                                                                                                         GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA 2028
                                                                                                GCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCCAGATGCAATT
ACCATTGGTGAAGATGTTAGCG 875
                                                                                                                                                                                                                                                                                                                     4.6%;
78.9%;
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Pred. No. 2.9e-15;
D; Mismatches 3C
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INFORMATION:

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CURRENT APPLICATION NUMBER: US/09/658,499
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 09/087,277
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: PCT/SE96/01558
PRIOR APPLICATION NUMBER: PCT/SE96/01558
PRIOR FILING DATE: 1996-11-28
PRIOR FILING DATE: 1995-11-29
PRIOR FILING DATE: 1995-11-29
PRIOR APPLICATION NUMBER: SE 9504272-7
PRIOR FILING DATE: 1995-11-29
PRIOR APPLICATION NUMBER: SE 9601506-0
PRIOR FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
SEQ ID NO 3
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US-09-087-277-1
                                                                     Sequence 1, Application US/09087277B Patent No. 6169226 GENERAL INFORMATION:
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LOCATION: (2)..(1393)
NAME/KEY: misc feature
LOCATION: (424)..(1150)
OTHER INFORMATION: Nucleotides 424, 89
OTHER INFORMATION: C, G or T.
NAME/KEY: misc feature
LOCATION: (422)..(424)
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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TITLE OF INVENTION: STARCH BRANCHING ENZYME
FILE REFERENCE: 003300-486
APPLICANT: EK, Bo
APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
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TYPE: DNA
ORGANISM: Unknown
FEATURE:
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PPLICANT: KHOSNOODI,
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LOCATION: (1148)..(1150)
OTHER INFORMATION: Amino acid 383 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (890)..(892)
OTHER INFORMATION: Amino acid
OTHER INFORMATION: or Phe.
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OTHER INFORMATION: Amino acid
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                      TCCATTGGTGAAGATGTAAGTG
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LARSSON, Hakan
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                                                                                                                                                                                                                                                                                                                                                                                                                                              4.6%;
78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 94; DB Pred. No. 2.9e 0; Mismatches
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ches 30;
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; FEATURE:
NAME/KEY: misc feature
; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein
US-09-087-277-1
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TITLE OF INVENTION: STARCH BRANCHING ENZYME I
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/087,2778
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PC7/8296/01558
EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
                                                                                                                                              Matches 112;
                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: mat_peptide
LOCATION: (333)..(2825)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430,
OTHER INFORMATION: n wherein n = A, C, G or T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (1896)...(1898)
OTHER INFORMATION: Amino a
OTHER INFORMATION: or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (189)..(2825)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Unknown OTHER INFORMATION: (branching enzyme II) f OTHER INFORMATION: (potato)
                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (285)..(287)
OTHER INFORMATION: Amino acid -16
OTHER INFORMATION: or Phe.
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LOCATION: (189)..(332)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1404)..(1406)
OTHER INFORMATION: Amino acid
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                                                                                                        1909 TTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGAT
                                                                                                                                                                Similarity
GCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCCAGATGCAATT 1859
                         GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA
                                                                       rtarcegreggartcacteggaactaceaggaatactreggactegeaactegatetegat
                                                                                                                                            Conservative
                                                                                                                                                                4.6%;
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                                                                                                                                              Score 94; DB
Pred. No. 4.2e
0; Mismatches
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TCCATTGGTGAAGATGTAAGTG 2050

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1860 ACCATTGGTGAAGATGTTAGCG 1881

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SOFTWARE: PatentIn Ver.
SEQ ID NO 1
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                                                                                                                     Matches 112;
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                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1898)
CHER INFORMATION: anino acid 522 is
OTHER INFORMATION: or phe.
NAME/KEY: misc_feature
LOCATION: (2154). (2156)
OTHER INFORMATION: Amino acid 608 is
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CURRENT APPLICATION NUMBER: US/09/658,499
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 09/087,277
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: PCT/SE96/01558
PRIOR FILING DATE: 1996-11-28
PRIOR FILING DATE: 1996-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: SE 9504272-7
PRIOR FILING DATE: 1995-11-29
PRIOR APPLICATION NUMBER: SE 9601506-0
PRIOR FILING DATE: 1996-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: EK, BO
APPLICANT: KHOSNOODI
APPLICANT: LARSSON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: mat_peptide
LOCATION: (333)..(2825)
NAME/KEY: misc_feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides 92, 20THER INFORMATION: n wherein n = A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Unknown Organism:beII gene OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum OTHER INFORMATION: (potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (189)..(2825)
NAME/KEY: sig_peptide
LOCATION: (189)..(332)
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                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino acid 366
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LOCATION: (1404)..(1406)
OTHER INFORMATION: Amino acid
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OTHER INFORMATION: or Phe.
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LOCATION: (285)..(287)
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1969 GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA 2028
                                                                                                                   Similarity 78.1
12; Conservative
                                                               TTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGAT 1968
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78.9%;
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358
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Pred. No. 4.2e-15;
O; Mismatches 30;
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APPLICANT:

APPLICANT:

Wang, Zi-Xuan

APPLICANT: Yamanouchi, Utako APPLICANT: Ishimaru, Lisa TITLE OF INVENTION: RICE GENE NUMBER OF SEQUENCES: 13

RESISTANT

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BLAST DISEASE

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street

Boston

MA

COUNTRY: USA ZIP: 02110-2804 COMPUTER READABLE FORM:

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LAIGUNI, Raghunath V.

APPLICANT: Ito, Laura Y.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 6200
LENGTH: 303
TYPE: DNA
ORGANITATION
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OTHER INFORMATION: Incyte ID No. 6476212 700351401H1

NAME/KEY: unsure

LOCATION: 245, 254, 265, 281, 294

OTHER INFORMATION: a, t, c, g, or other

US-09-313-294A-2200
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                                                                                                                                     RESULT 13
                                                                                    Sequence 3 Patent No.
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Best Local
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                                                                  GENERAL INFORMATION:
                                   APPLICANT:
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                                                                                       , Application US/09330330 6274789
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Yano, Masahiro
Iwamoto, Masao
Iwamoto, Yuichi
Katayose, Yuichi
Sasaki, Takuji
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71.18;
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Pred. No. 1.9e
0; Mismatches
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l.9e-15;
nes 50;
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Sequence 25, Application US/09257894
Patent No. 6376749
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06501/032001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 10
FILING DATE: 12-JUN-1998
ATTORNEY/AGENT INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Nattalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: Ro. 6376749el Starches via Modification
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                      E: E. I. du Pont de Nemours and Company 1007 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATGTTGTAGATATCAGCACATTTTTCTATAGACTTGGTCAAATATAGAGAAGTTTG 1139
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12-JUN-1998
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Pred. No. 1.2e-09;
0; Mismatches 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/09257894 Patent No. 6376749 GENERAL INFORMATION:
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Best Local Similarity
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,
APPLICATION NUMBER: 09/091,
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Majarian, William R. REGISTRATION NUMBER: 41.173 REFERENCE/DOCKET NUMBER: 81.183 TELECOMMUNICATION INFORMATION: TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: JUNE 10, 19
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: Microsoft Windows SOTTWARE, Version 7.08 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
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STRANDEDNESS: SI
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                                                                                                                                                                                     APPLICATION NUMBER: US/09/257,894 FILING DATE:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      955 GGCACACCAGAGGACCTCAAATATCTTGTTGATAAGGCACACAGTTTGGGTTTTGCGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 GGAACTCCAGAGGACTTAAAATCCTTGATCGATAGAGCACATGAGCTTGGTTTGCTTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 TTGTTGTTGGCTTGTTCCAGGTACCATGTTACTAATTTTTTTGCACCAAGTAGCCGTTTT
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: Delaware
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1007 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Broglie, Karen E.
Klein, Theodore M.
Hubbard, Natalie L.
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69.3%;
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Pred. No. 3.7e-09;
0; Mismatches 43;
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밁 Ş 밁 US-09-330-330-3

Query Match Best Local Similarity

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GENERAL INFORMATION:

COUNTRY:

ADDRESSEE:

Wilmington

Delaware

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Page 8
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REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
FELECOMMUNICATION INFORMATION:
TELEPHAN: 302-773-0164
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1865 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: lines
OLECULE TYPE: CDNA
US-09-257-894-20
Search completed: April 10, 2004, 14:13:12  
    Job time : 150.768 secs
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                                                                                                                                            1011 GECACACCÁGÁGGÁCCTCÁÁATATCTTGTTGÁTÁAGGCÁCÁCAGTTTGGGTTTTGCGAGTT 1070
                                                                         1071 CTGATGGATGTTGTCCATAG 1090
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                           2025
139.4
1126.2
1112.4
1112.5
1105.2
105.2
105.1
105.1
101.8
101.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:*

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18: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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Gapop 10.0 , Gapext 1.0
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Match Length
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                                               ccgaagataaattcatatgc.....cattggtgaagatgtaagtg 2050
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10621.793 Million cell updates/sec
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                                                                                            12 US-10-434-893A-3

12 US-10-434-893A-1

12 US-10-434-893A-3

15 US-10-260-238-1027

12 US-10-260-238-253

15 US-10-260-238-2253

15 US-10-260-238-2253

15 US-10-260-238-2253

16 US-10-260-238-2253

17 US-10-260-238-2253

18 US-10-260-238-2253

19 US-10-260-238-2253

10 US-10-260-238-2424
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Sequence 3, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 1027, Ap
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 253, Appli
Sequence 14, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
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US-10-434-893A-3

Sequence 3, Application US/10434893A

Publication No. US20940060083A1

Publication No. US20940060083A1

Publication No. US20940060083A1

APPLICANT: Ahmed Regina

APPLICANT: Matthew Kennedy Morell

APPLICANT: Sadequr Rahman

ITILE OF INVENTION: Barley with altered branching enzyme activity and starch and starting OF INVENTION: containing products with an increased amylose content FILE REFERENCE: 69425

CURRENT ETLING DATE: 2003-05-09

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin version 2.1

SOFTWARE: Patentin version 2.1

TYPE: DNA

ORGANIAN: Accidence tameshii
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; OTHER INFORMATION: SSBEIIa gene
US-10-434-893A-3
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                                                                                                                              Query Match 98.8%; Score 2025; I Best Local Similarity 99.8%; Pred. No. 0; Matches 2049; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                       ORGANISM: Aegilops tauschii
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(11476)
OTHER INFORMATION: n is a,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GGATACAATGCAGTGCAGATAATGGCAATCCAGGAGCATTCATACTATGCAAGCTTTTGGG
                                                                               CCGAAGATAAATTCATATGCTAATTTTAGGGATGAGGTGTTGCCAAGAATTAAAAGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 US-10-056-454A-19
14 US-10-254-534-1
15 US-10-256-454A-13
14 US-10-256-454A-13
14 US-10-056-454A-13
15 US-10-056-454A-13
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19 US-09-887-576-830
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                                                                                                                                                                         DB 12; Length 11476;
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Result No.

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1017 CATCTACAACACCAAATTACTTTGATCAGARTTAACAATTTTTATTATTATTAGCAC 1076	TATTCACACATCCATTTTTTCTGTATACAC-TCTTCACCCATTTGGAGCTATTACATC THICLEANATCCATTTTTTCTGTATACAC-TCTTCACCCATTTGGAGCTATTACATC TATTCACACATCCATTATACTTTTTCTGTATACACCTTTTATTAGATATACTCATTTCACACCTTTTCACACCTTTTCACACCTTTTAGATACTCATTTCACACCCATTTCACACCTTTTAGATATACTCATTTAGATATACTCTTTATTAGATATACTCATTTCACACCCATTTCACACCCATTTCACACCCATTTCACACCCACCTTTTATTA
US-10-434-893A-1 US-10-434-893A-1 Sequence 1, Application US/10434893A Sequence 1, Application No. US20040060083A1 Publication No. US20040060083A1 GENERAL INFORMED Regina APPLICANT: And Regina APPLICANT: Matthew Kennedy Morell APPLICANT: Sadequr Rahman TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and TITLE OF INVENTION: containing products with an increased amylose content FILE REFERENCE: 69425 CURRENT APPLICATION NUMBER: US/10/434,893A	De CORDINATION CONTROLLE DE LA

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CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 2.1
SEQ ID NO 1
LENGTH: 2554
TYPE: DNA
ORGANISM: Hordeum vulgare
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WS-10-434-893A-3/c
US-10-434-893A-3/c
; Sequence 3, Application US/10434893A
; Publication No. US20040060083A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                          ; OTHER INFORMATION: SSBEIIa gene US-10-434-893A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ahmed Regina
APPLICANT: Matthew Kennedy Morell
APPLICANT: Matthew Kennedy Morell
APPLICANT: Matthew Kennedy Morell
APPLICANT: Sadequr Rahman
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch:
TITLE OF INVENTION: containing products with an increased amylose content
FILE REFERENCE: 69425
CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 2.1
SEQ ID NO 3
LENGTH: 11476
TWO BERT OF SERVER OF S
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                                                                                                           Query Match 6.2%; Score 126.2; DB 12; Length Best Local Similarity 64.6%; Pred. No. 2.4e-18; Matches 188; Conservative 0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Aegilops tauschii
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(11476)
OTHER INFORMATION: n is a, c,
FEATURE:
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911 ATGTTACTTCCCTGTTGAATTCATTTGAACATATTACTTAAAGTTCTTCATTTGTCCTAA
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             RESULT 5
US-10-434-893A-4
; Sequence 4, Application US/10434893A
; Publication No. US20040060083A1
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APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 1027
LENGTH: 1442
TYPE: NNA
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Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
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US-10-260-238-1027
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US-10-260-238-1027
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APPLICANT:
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                        ATTCAACTATGGGAGTTGGGAAGTATGTAGCTCT 1526
                                                                                                             TGATACACATTACTTCCACGGGGGCCACGCGGCCATCATTGGATGTGGGGATTCTCGTCT
                                                                                                                                                                      TGTTCACAGCAGCCATGCGTCAAATAATACCCTAGATGGGTTGAACGGTTTTGATGGTAC
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TTTCAACTATGGGAATTGGGAAGTTCTAAGATTT 476
                                                                                     AGATACGCATTACTTTCATAGTGGTTCACGCGGCCATCATTGGATGTGGGATTCTCGCCT
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Goff, Stephen A.
Katagiri, Fumiyaki
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Provart, Nicholas
Ricke, Darrell
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TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 2253
LENGTH: 2000
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SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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APPLICANT: Matthew Kennedy Morell
APPLICANT: Sadequir Rahman
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and
TITLE OF INVENTION: containing products with an increased amylose content
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CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
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NAME/KEY: MISC FEATURE
LOCATION: (1)...(6550)
OTHER INFORMATION: n is a, c, g or t
FEATURE:
OTHER INFORMATION: partial SSBEIIb gene
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TYPE: DNA
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Goff, Stephen A
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Ricke, Darrell
                                                                                                                                                                                                                                                                                                             Katagiri,
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74.6%;
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Pred. No. 3.1e-15;
0; Mismatches 48
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US-10-260-238-2253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Word SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 172;
                                                                                                                                                                                                                                           Matches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 2443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1120
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                                                          TCCATTGGTGAAGATGTAAGTG 2050
                        ACCATTGGTGAAGATGTTAGTG
                                                                                              GCAGTGGTTTACTTGATGCTGGTAAATGATCTAATTCATGGACTTTATCCTGAGGCTGTA
                                                                                                                                                                                                                                             Conservative
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; TYPE: DNA
; TYPE: DNA
; PEATURE:
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2443)
; OTHER INFORMATION: SBEII modified region
US-10-397-954A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pearlstein, Richard W.
APPLICANT: Broglie, Karen E.
APPLICANT: Hines, Christopher F.
TITLE OF INVENTION: Maize Starch Containing Eleptic Reference: BB1510 UN AND CURRENT EPILICATION NUMBER: US/10/397,954A
CURRENT EPILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: 60/368,387
PRIOR APPLICATION NUMBER: 60/368,387
PRIOR PILING DATE: 2002-03-27
PRIOR PILING DATE: 2002-03-27
PRIOR FILING DATE: 2002-05-16
NUMBER: MISCOCFT WEST OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10397954A Fublication No. US20030221220A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1000 ATTGGAAAATATATCAACATCTACAACACCAAATTACTTTGATCAGATTAACAATTTTTA 1059
                                                                                                                                  1909 TTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTTGGATTTGCTACTGATGTTGAT 1968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                817 CATATTATAAATCGCTTTGACTTTTTCCTAATCAAACTTCTTTACATCTGACCAAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             940 CATATTACTTAAAGTTCTTCATTTGTCCTAAGTCAAACTTCTTTAAGTTTGACCAAGTCT
                                         GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA 2028
                                                                                         TTACAAGTAACATTTACGGGGAACTTCAATGAGTATTTTGGCTTTGCCACCGATGTAGAT 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÀAGGÁGTÁTTTÁÁTÁCT 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITTATTATATAGCACATCTTTGATGTTGTAGATATCAGCACATTTTTCTATAGACTTG 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAGGAAAATGTAGCAGCATCTACAACACCAAATTAGTTTATTAAATGTAACATTGAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGGAACATCAAATAAT 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCAAACTTTAAAAAAGTTTGACAAAGGAAAAAGTCAAAGCGACTTATAATATGAAATGG 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.9%;
                                                                                                                                                                                                      5.1%;
83.8%;
                                                                                                                                                                           Score 105.2; DB 1
Pred. No. 7.8e-14;
0; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 110.6; DB 1
Pred. No. 3.9e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elevated Amounts of Actual Amylose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 15;
                                                                                                                                                                                                                              DB 15;
                                                                                                                                                                                   23;
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1148
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GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Allen, Steve
APPLICANT: Beckles, Diane M.
APPLICANT: Beckles, Diane M.
APPLICANT: Butler, Karla
APPLICANT: Pearlstein, Rich
TITLE OF INVENTION: Starch Branching Enzyme IIb
FILE REFERENCE: BB1439 US NA
FURRENT APPLICATION NUMBER: US/09/792,127
CURRENT APPLICATION NUMBER: US/09/792,127
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/186098
PRIOR FILING DATE: 2000-03-01
NUMBER OF SEQ ID NOS: 5
В
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US-09-792-127-3
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APPLICANT: Beckles, Diane M.
APPLICANT: Beckles, Diane M.
APPLICANT: Butler, Karla
APPLICANT: Pearlstein, Rich
TITLE OF INVENTION: Starch Branching Enzyme IIk
FILE REFERENCE: BB1439 US NA
CURRENT APPLICATION NUMBER: US/09/792,127
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/186098
PRIOR FILING DATE: 2000-03-01
                                                                                                                                                                                      ; SEQ ID NO 3; LENGTH: 3039; TYPE: DNA; ORGANISM: Triticum aestivum US-09-792-127-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-792-127-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09792127
Patent No. US20020002713A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                            Query Match 5.1
Best Local Similarity 82.8
Matches 120; Conservative
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SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 2559
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Local Similarity 82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1442 TTACTTCCACGGTGGTCCACGCGGCCATCATTGGATGTGGGATTCTCGTCTATTCAACTA 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1382 CAGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGCCACTGATACACA 1441
1307 CAGTCACGCGTCAAATAATACCTTGGACGGGTTGAATGGTTTTGATGGCACGGATACACA 1366
                                             1382 CAGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACA 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    827 CAGTCACGCGTCAAATAATACCTTGGACGGGTTGAATGGTTTTGATGGCACGGATACACA
                                                                                                                                                                                                                                                                                                               Microsoft Office 97
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                                                                                                                   5.1%;
82.8%;
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                                                                                          Score 105; DB 9; I
Pred. No. 9.7e-14;
0; Mismatches 25;
                                                                                                                                         Length 3039;
                                                                                               Indels
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US-10-260-238-2253/c
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US-10-434-893A-2
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Publication No. US20040060083A1

Publication No. US20040060083A1

GENERAL INFORMATION:

APPLICANT: Ahmed Regina
APPLICANT: Matthew Kennedy Mozell
APPLICANT: Sadequr Rahman

TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and ITITLE OF INVENTION: containing products with an increased amylose content FILIS REFERENCE: 69425

CURRENT FILING DATE: 2003-05-09

NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.0%; Score 101.8; DB 12; Length 2780; Best Local Similarity 77.0%; Pred. No. 5.1e-13; Matches 124; Conservative 0; Mismatches 37; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 2.1
SEQ ID NO 2
LENGTH: 2780
TYPE: DNA
ORGANISM: Hordeum vulgare
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: SSBEII'D CDNA
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                                                                                              1235 GTCACGCATCAAGTAATACCTTGGACGGTTTGAATGGTTTT 1275
                                                                                                                                                                                                                                     350 AATCCTTGATCGATAGAGCACATGAGCTTGGTTTGCTTGTTCTTATGGATATTGTTCATA 409
                                                                                                                                                                                                                                                                                                                              290 GGTACCATGTTACTAATTTTTTTGCACCAAGTAGCCGTTTTGGAACTCCAGAGGACTTAA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTACCATGTTACCAATTTCTTTGCACCAAGTAGCCGTTTTGGGTCCCCAGAAGATTTAA 1174
                                                                                                                                       GGTAATTAGTCCAATTTAATTTTAGCTGTTTTACTGTTTAT 450
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Sequence 2253, Application US/10260238

Publication No. US20040016025A1

GENERAL INFORMATION:

APPLICANT: Budworth, Paul R.
APPLICANT: Briggs, Steven P.
APPLICANT: Briggs, Steven P.
APPLICANT: Glazebrook, Jane
APPLICANT: Glazebrook, Jane
APPLICANT: Katagiri, Funiyaki
APPLICANT: Katagiri, Funiyaki
APPLICANT: Kreps, Joel
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Thurention: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 6011-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/325,277
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; TYPE: DNA; ORGANISM: Oryza sativa US-10-260-238-2253
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                                                                                                                    NAME/KEY: CDS
LOCATION: 145..2790
LOCATION: DESCRIPTION: SEQ ID NO: 14:
US-10-056-454A-14
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Publication No. US20030166919A1

GENERAL INFORMATION:

APPLICANT: National Starch and Chemical Investment Holding Corporation

TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition

NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 2253
LENGTH: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Sim Matches 165;
                                       Matches 129;
                                                                             Query Match
                                                                                                                                                                                                                                   INFORMATION FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3033 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1119
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: US/10/056,454A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1050 CATATTATAAGTCGCTTTGACTTTTTCCTTTGTCAAACTTTTTTAAAGTTTGACCAAGTT
1865 TIGGAAGIGATIATIATITATITICITICIAAGITIGITICITGITICIAGATGACATITA 1924
                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  999 TATTGGAAAATATATCAACATCTACAACACCAAATTACTTTGATCAGATTAACAATTTTT 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTTTATTATTAGCACATCTTTGATGTTGTAGATATCAGCACATTTTTCTATAGACTT 1118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGGAGTATCAAGT 797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGTTACATTTAATAAACTAATTTGGTGTTGTAGATGCTGCTACATTTTCCTATAAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America ZIP: 19720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Delaware
                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITY: Newcastle
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                                       Conservative
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                                                          4.6%;
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bred. No. 5.9e-13;
bred. No. 5.9e-88;
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                                       0
                                     Score 94.8; DB 14;
Pred. No. 2.2e-11;
D; Mismatches 57;
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                                                                             Length 3033;
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US-10-254-534-3
; NAME/KBY: misc feature
; LOCATION: (1148)..(1150)
; OTHER INFORMATION: Amino
US-10-254-534-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/10/254,534
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US/09/087,277
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: PCT/SE96/01558
PRIOR FILING DATE: 1996-11-28
PRIOR APPLICATION NUMBER: SE 9504272-7
PRIOR APPLICATION NUMBER: SE 9601506-0
PRIOR APPLICATION NUMBER: SE 9601506-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
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                                                                                                                                                                                  PEATURE:
NAME/KEY: misc feature
LOCATION: (422)..(424)
OTHER INFORMATION: Amino a
FEATURE:
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APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II
                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Unknown Organism:bell gene fragment OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum OTHER INFORMATION: (potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                                                                                       NAME/KEY: misc_feature
LOCATION: (890)..(892)
OTHER INFORMATION: Amino acid
OTHER INFORMATION: or Phe.
                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature LOCATION: (424)...(1150) COCHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A, OTHER INFORMATION: C, G or T.
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LOCATION: (2)..(1393)
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LARSSON, Clas-Tomas
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Query Match Best Local Similarity

4.6%; 78.9%;

Score 94; Pred. No.

DB 14; 2.3e-11;

Length 1393;

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; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-2424
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                                                                                                                                                                                                                                                                                                                                                  Query Match 4.6%;
Best Local Similarity 62.0%;
Matches 165; Conservative
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
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                                                                            AGAGACATATATAATAATTATAATACTAAATTAGTTTCATCAAATCAATAA-TTGAA
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GGGAACATCAAATAATATAGATAGAT 1205
                                        ATCAAACTTAAAGCAGTTTGGCTTTGATCAAAGTCAAAACGTCTTAAAACCTGAAACGGA
                                                                                                                    TATATTTTTATAATAATTTGTCTTGGGTTGAAATGTTACTACTTTTTTCTACAAACTTG 690
                                                                                                                                                       TTTTATTATTAGCACATCTTTGATGTTGTAGATATCAGCACATTTTTCTATAGACTTG
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Ricke, Darrell
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iri, Fumiyaki
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RESULT 15
US-10-056-454A-16
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Search completed: April 10, Job time: 729.03 secs
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SEQUENCE CHARACTERISTICS:
LENGTH: 2576 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/10056454A Publication No. US20030166919A1
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Best Local Similarity 78.9%;
Matches 112; Conservative
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CORRESPONDENCE ADDRESS: ADDRESS: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
                                                                                            1591
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                                                                                                                                                                                                                                                                                                                          1909 TTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTTGGATTTGCTACTGATGTTGAT 1968
                                                                                                                                      2029 TCCATTGGTGAAGATGTAAGTG 2050
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                                                                                            ACCATTGGTGAAGATGTTAGCG 1612
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STATE: Delaware
                                                                                                                                                                                      GCTGTTGTGTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCAGATGCAATT 1590
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                          2004, 20:07:35
                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Score 94; DB 14; Length 2576; Pred. No. 3.2e-11;
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Minimum DB
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Perfect score:
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Maximum Match
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                                                     250.8
                                                                                                                                     Score
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CC362748 CC362748.1 GI:30832148
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
                                                                                                                                                                                        Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUHLB23TB
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                                                                                      301-838-5843
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BU970967 HB16D15r
CA292638 SCRLFLB02
CA202517 SCRFFL102
AY109521 Zea maye
BM660711 952041B07
CA188662 SCCCAM2CO
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A0846560 hp58611.9
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AG213031 Oryza sat
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CA191146 SCCCRT2CO
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                                           GTTCATAGGTA 360
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Email: bharti@waksman.rutgers.
Seq primer: T7
Class: BAC ends
High quality sequence start: 1
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Zea mays subsp. mays (maize)

Zea mays subsp. mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.
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Tel: 732 445 3801
Fax: 732 445 5735
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The Plant Genome Initiative
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                                                                                                                                                                   TGTTCCAGGTACCATGTTACTAATTTTTTTGCACCAAGTAGCCGTTTTGGAACTCCAGAG
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                                           GACTTAAAATCCTTGATCGATAGAGCACATGAGCTTGGTTTGCTTCTTATGGATATT
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GTTCATAGGTA 413
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/clone_lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII;
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/cultivar="B73"
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71.0%;
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Matches 241; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum (bread wheat)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (03-JUL-2002) to the EMBL/GenBank/DDBJ databases. Barker G., Institute of Arable Crop Research, Long Ashton, Bristol BS41 9AF United Kingdom.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2002 (Rel. 02-SEP-2002 (Rel.
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    CTCCATGATGTATACTCACCATGGATTACAAGTAA 1717
                                                 <u>AAACGCGAGATGGTGGCTTGAAGAATATAAGTTTGATGGATTTCGATTGATGGGGTGAC</u>
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/tissue_type="maternal tissue (minus endosperm
/clone_lib="e:411"
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/mol_type="mRNA"
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/cultivar="mercia"
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72, Last updated, Version
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P., Edwards
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
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Fax: 039482-5595
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Radchuk,V., Zhang,H., Weschke,W.,
Barley ESTs from developing seeds
Unpublished (2002)
Contact: Stein Nils
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HB21K16r BC Hordeum vulgare subsp. vulgare
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Insert Length: 476 Std Error:
Plate: 21 row: K column: 16
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                                                                                                                      GGGAGTTGGGAAGTATGTAGCTCTGACTTCTGTCACCATAFTTGGCTAACTGTTCCTGTT
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                                                                                                                                                                                                                                                                        AGTCATTCGTCAAATAATACCCCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACAT
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=Tvector: pBluescript SK+; Site_1: EcoRI (5'-end of CDNA); Site_2: KhoI (3'-end of CDNA); developing caryopsis, 8-15 DAP(days after pollination) Due to a cloning arrefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PSII). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
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/dev stage="8-15 DAP (days after pollination)"
/lab_host="XL10-Gold"
/clone_lib="BC"
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/cultivar="barke"
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/db_xref="GABI:237282"
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                                                                                                                                                                                                                                                                                                                                                                        Score 139.4; DB
Pred. No. 1e-16;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13;
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Best Local S
Matches 241
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89
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Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IFK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases 1 to 537)

1 (bases 1 to 537)
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HB03P08r BC Hordeum vulgare
5-PRIME, mRNA sequence.
BU967331
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Barley ESTs from developing seeds
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: stein@ipk-gatersleben.de
Insert Length: 537 Std Error:
Plate: 3 row: P column: 8
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EST.
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                       TACTTCCACGGTGGTCCACGCGGCCATCATTGGATGTGGGATTCTCGTCTATTCAACTAT 1502
AGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTTCGATGGCACTGATACACAT
                                                                                                                                       AGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTTTCGATGGCACTGATACACAT 1442
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                                                                                                                                                                                                                 6.8%;
ilarity 71.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                      /note="Nector: pBluescript SK+; Site_1: EcoRI (5'-end of /note="Nector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); developing caryopsis, 8-15 DAP(days after pollination) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. Bam#I, Sali,PStI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="developing caryopsis"
/dev_stage="8-15 DAP (days after pollination)"
/lab_bost="XILL-Gold"
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1. .537
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/db_xref="GABI:232152"
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/cultivar="barke"
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/clone="HB03P08"
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                                                                                                                                                                                                                    Score 139.4; DB 13;
Pred. No. 1e-16;
0; Mismatches 6;
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vulgare
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cDNA clone HB03P08
                                                                                                                                                                                                                          Indels 88;
                                                                                                                                                                                                                                                                            Length 537;
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Wheat functional genomics - Glenlea developing seeds cDNA libraries unpublished (2002)

Contact: Dr. Sylvie Cloutier
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9

Tel: (204) 983-2340

Fax: (204) 983-240

Fax: (204) 983-240

Fax: (204) 983-240

Fax: (204) 983-250

Fax: (204) 983-250

Fax: (204) 983-250

Fax: (204) 983-260

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        202 GCGGTCGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA
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476 bp mRNA linear EST 03-MAY-2002
TaE15032A02R TaE15 Triticum aestivum cDNA clone TaE15032A02R, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
BQ245037
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Triticum aestivum
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                                                                                                                   TTCTAGATGACATTTACTGGGAACTATGGCGAATATTTTGGATTTGCTACTGATGTTGAT 1968
                                      GCGGTAGTTTACTTGATGCTGGTCAACGATCTAATTCATGGACTTTATCCTGATGCTGTA 2028
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                                                                                                                                                                                                                                6.5%; ilarity 96.5%; Conservative
                                                                                                                                                                                                                                                                                                                                                                     /clone="Tabli332A02R"
/clone="Tabli332A02R"
/dey_stage="15 days after anthesis"
/lab_host="E. coli_DH10B"
/clone="coli_DH10B"
/clone="tib="Tabli5"
/clone="tib="Tabli5"
/note="tib="Tabli5"
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/note="tib="Tabli5"
/note="tib="tib="tib="tib"
/note="tib"
/note i: Noti; Site 2: MluI; mRNA obtained from wheat seeds of cultivar Glenlea 15 days post-anthesis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="Glenlea"
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Best Local Similarity
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                                                                                                                                                          BU98646.1 GI:24237592
EST.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 623)
Radchuk, V, Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
Barley ESTs from developing seeds
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B198646 623 bp
HF12102r HF Hordeum vulgare subsp.
5-PRIME, mRNA sequence.
BU986646
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Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: stein@ipk-gatersleben.de
Insert Length: 623 Std Error: 0.00
Plate: 12 row: I column: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: M13rev
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     GGGAGTTGGGAAGTATGTAGCT 1524
                                                                                 TACTTCCACGGTGGTCCACGGGGCCATCATTGGATGTGGGATTCTCGTCTATTCAACTAT 1502
                                                      TACTTCCACGGTGGTCCACGTGGCCATCATTGGATGTGGGATTCTCGTCTGTTCAACTAT 582
                                                                                                                                                                                                                                                            6.5%; Score 134; DB 13; Length 623; ilarity 96.5%; Pred. No. 1.1e-15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="HF"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Geveloping caryopsis, 16-25 DAF(days after flowing) Due to at cloning carefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI,PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable.Average insert size is 940 bp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="caryopsis"
/dev_stage="developing caryopsis, 16-25 DAF (days
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:112509"
/clone="HF12I02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sub_species="vulgare"
/db_xref="GABI:246586"
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Matches 344; Conserv
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        1529 CTTCTGTCACCATATTTGGCTAACTGTTCCTGTTAATCTGTTCTTACACATGTTGATATT 1588
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 610)
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGAGTTGGGAAGTATTAAGAT 604
                                                                                              GTGGGATTCTCGTCTATTCAACTATGGGAGTTGGGAAGTA;-----TGTAGCTCTGA 1528
                                                           GTGGGATTCTCGCCTTTTCAACTATGGGAATTGGAAGTAAAGGAACACGTTAATCGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 442.
Location/Qualifiers
                                                                                                                                                                                                                                                                                 / clone "haxbole3901r"

/clone inbxbole3901r"

/clone lib="CUGI Rice BAC Library"

/clone libe "CUGI Rice BAC Library"

/clone library specific library source of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monococyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of genome of rice, three times larger than that of genome sequencing of rice, we have constructed a BAC library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
                                                                                                                                                               6.5%; Score 133.2; DB 28; Length llarity 59.1%; Pred. No. 1.5e-15; Conservative 0; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
|mol type="genomic DNA"
|/strain="Japonica"
|cultivar="Nipponbare"
|/db_xref="taxon:39947"
                                                                                                                                                                                                                      Length 610;
                                                                                                                                                                        70;
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                                                                                                                                  93, rue Henri Rochefort 91025 EVRY CEDEX France Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                                                                                                                                     Genoplante, a major partnership 
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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CD890409.1 GI:32659746
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G118.114J06F010718 G118 Triticum
                                                                                                                                                                                                                                                        Contact: Genoplante
                                                                                                                                                                                                                                                                                                   Genoplante.
                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; Pooideae; Triticeae; Triticum.
1 (bases 1 to 621)
                                                                                                                                                                                                                                                                                                                                                                                       Triticum aestivum (bread wheat)
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                  /tissue_type="grain
pollination)"
                                                                         /mol_type="mRNA"
/cultivar="recital"
                                               /clone="G118114J06"
                                                             db_xref="taxon:4565"
                                                                                                       organism="Triticum aestivum'
 clone_lib="G118"
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ATTGTTCATAGTCATTCGTCAAATAATACCCTTGACGGTTTGAATGGTT
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136; Conservative
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1 (bases 1 to 678)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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AV939010.1 GI:18234807
                                                                                                                                                                                                                               Similarity
                                                                                                                             GCGAGCTTTGGGTACCATGTTACTAATTTTTTTGCACCAAGTAGCCGTTTTGGAACTCCA
                                                                        GAGGACTTAAAATCCTTGATCGATAGAGCACATGAGCTTGGTTTGCTTGTTCTTATGGAT
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ATTGTTCATAGGTAATTAGTCCAATTTAATTTTAGCTGTTTTACTGTTT
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81-559-81-6855
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                /tissue_type="top three leaves"
/dev_stage="adult, heading stage"
/clone_lib="K. Satco unpublished cONA library,
adult, heading stage top three leaves"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="H602"
                                                                                                                                                                                                                                                                                                                                                                                                    clone="bah20e24"
                                                                                                                                                                                                                                                                                                                                                                                                                            sub_species="spontaneum"
db_xref="taxon:77009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Hordeum vulgare subsp.
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Pred. No. 3.9e-1
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ches 6;
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618 bp mRNA linear l
SCRLPL8025G06.g FL8 Saccharum officinarum cDNA clone
5', mRNA sequence.
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Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
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Radchuk, V., Zhang, H., Weschke, W.,
Barley ESTs from developing seeds
Unpublished (2002)
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
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HB16D15r BC Hordeum vulgare;
5-PRIME, mRNA sequence.
BU970967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Hordeum vulgare subsp. vulgare"
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/dev stage="8-15 DAP (days after pollination)"
/lab host="XII0-Gold"
/clone_lib="BC"
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/db_xref="taxon:112509"
/clone="HB16D15"
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cDNA clone HB16D15
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Spermatophyta; Milopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.

El (bases 1 to 618)
Clade; Panicoideae; Andropogoneae; Saccharum.

El (bases 1 to 618)
Charcie, L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact; Arruda P
Contact; Arruda P
Contact; Arruda P
Contact; Arruda P
Contact; Arruda Bollogia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Coatxa Poestal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1039
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 025 row: G column: 06
Seq primer: T7 Promoter Primer.

Seq primer: T7 Promoter Primer.
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                                                                                                  SCRFFI1027B04.g FL1
5', mRNA sequence.
CA202517
CA202517.1 GI:3523
Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta Magnoliophyta; Tiliopsida: Poales: Poaceae: PACCAD
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/mol_type="mRNA"
/db_xref="taxon:4547"
/db_xref="taxon:4547"
/clone="SCRLEHB025G06"
/lab_host="DH10B"
/clone=lib="FL8"
/note="Organ: Developing inflorescence and rachis
/note="Organ: Developing inflorescence and rachis
/note="Organ: Developing inflorescence and rachis
/note=scence and rachis (10cm-long)). CDNA was prepared
inflorescence and rachis (10cm-long)). CDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.lad.io.unicamp.br/public"
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marum officinarum
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Clone distribution: clone distribution information cathrough the Brazillan Clone Collection Center (BCCC) http://www.bcccenter.fcav.unesp.br
Plate: 027 row: B column: 04
Seq primer: T7 Promoter Primer.
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Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
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Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
                                                                                                          Zea mays
Zea mays
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                   HTC.
                                                                                                                                                                                                                                   AY109521 2766 bp
Zea mays CL1245_1 mRNA sequence.
AY109521
AY109521.1 GI:21213273
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                                      Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V. Maize Mapping Project/DuPont Consensus Sequences for Design of
                  Maize Mapping Project/DuPont
Overgo Probes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACTTCCATGGTGGTCCACGGGGCCATCATTGGATGTGGGATTCTCGCCTATTCAATTAT 307
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/mol_type="mRNA"
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Pred. No. 1.2e-13;
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Matches 133
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Submitted (25-APR-2002) Maize Mapping Project, University of Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones, these are publicly available from ZDBB and may be found by BLAST searching at MSL, maizemap.org; ZDBB, www.rmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of t. maize CDNA sequences is either Virginia Walbot, Stanford or Pat maize CDNA sequences is either Virginia Walbot, Stanford or Pat
                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays
Zea mays
                                                                                                                                                                  Contact: Walbot V
Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea
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Email: walbot@stanford.edu
Plate: 952041 row: B column:
Cocation/Qualifiers
1...399
                                                                                            855 California Ave,
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                        Unpublished (1999)
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Maize ESTs from various cDNA libraries sequenced at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mapping Project"
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/db_xref="MaizeDB:630161"
/db_xref="texcon:4577"
/db_xref="Maize Mapping Project/DuPont Cornsensus
/clone_lib="Maize Mapping Project/DuPont Cornsensus
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Search completed: April 10, 2004, 14:06:33 
Job time : 5423.32 secs
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/clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"
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/mol type="maNS (Black Mexican Sweet)"

/db_xref="taxon:4577"

/db_xref="taxon:4577"

/tissue_type="suspension culture"

/dev_stage="mixed logarithmic and stationary growth
phases"
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16: em fun:*

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23: em bus:*

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25: em hug inv:*

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11057.263 Million cell updates/sec
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number of results predicted by chance to have

REFERENCE AUTHORS TITLE

Li,Z., Morell,M. and Rahman,S. Regulation of gene expression in

plants

Aegilops tauschii Aegilops tauschii Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Eukaryota, Magnoliophyta, Liliopsida, Poales, Poaceae, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,

RESULT 1
AXO31271
LOCUS
DEFINITION
ACCESSION
VERSION
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KEYWORDS
SOURCE
ORGANISM

AX031271 Sequence 10: AX031271 AX031271.1 (

11463 bp from Patent WO9914314.

DNA

linear

PAT 20-SEP-2000

ALIGNMENTS

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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N FIELDER LITD (AU); LIZ ZHONGYI (AU); MORELL MATTHEW (AU)
SADEQUR (AU); UNIV AUSTRALIAN (AU); COMMW SCIENT IND RES
U); GROUPE LIMAGRAIN PACIFIC PTY L (AU)
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/mol_type="unassigned DNA"
/db_xref="taxon:37682"
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Aegilops tauschii

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Aegilops.

1 (bases 1 to 11475)

Rahman, S., Regina, A., Li, Z., Mukai, Y., Yamamoto, M.,

KOSAT-Hashemi, B., Abrahams, S. and Morell, M.K.

Comparison of starch-branching enzyme genes reveals evolutionary

relationships among isoforms. Characterization of a gene for

relationships among isoforms. The wheat genome donor Aegilops

starch-branching enzyme IIa from the wheat genome donor Aegilops
                                                                                                Rahman,S., Regina,A., Li,Z., S
Direct Submission
Submitted (18-JAN-2001) Plant
Canberra, ACT 2601, Australia
Location/Qualifiers
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Aegilops tauschii starch
AF338431 GI:13447949
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                    /organism="Aegilops tauschii"
/mol type="genomic DNA"
/db xref="texon:37682"
/chromosome="2"
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Zhu,T., Cheng,W., Briggs,S., Cooper,B., Goff,S.A., Glazebrook,J., Katagiri,F., Kreps,J., Provart,N. ar Identification and characterization of plant genes Patent: WO 03000905-A 1018 03-JAN-2003;
                                                                                                                                                             Triticum aestivum (bread wheat)
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Matches 370; Conserv
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1 (bases 1 to 2853)

1 (bases 1 to 2853)

Willmitzer,L., Kroger,C., Lutticke,S. and Lorz,H.

Willeotide sequences encoding enzymes that alter the

Concentration and composition in plants

Patent: US 6570066-A 3 27-MAY-2003;

Patent: US 6570066-A 3 1616ers
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Sequence
AR340173
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                                                                                                             27.5%; Score 370; DB 6; ilarity 100.0%; Pred. No. 3.3e-93; Conservative 0; Mismatches 0;
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/db_xref="taxon:4565"
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/mol_type="genomic DNA"
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from patent US 6570066.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-AUG-1996) University of Hamburg, Institute of General Botany, Centre of Applied Molecular Biology, AMP II, Ohnhorststr. 18, Hamburg 22609, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyte; Magnoliophyta; illio
Pooideae; Triticeae; Triticum.
1 (bases 1 to 2853)
Kroeger,C., Loerz,H. and Luetticke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
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Triticum aestivum
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Location/Qualifiers
A-alpha-D-(1, -alpha-D-glucanotransferase"

/protein_id="AAB17086.1"

/protein_id="AAB17086.1"

/db_xref="G1:1620662"

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PKIRMTPSGVKDSISAWIKFSVQAPGEIFPNGIYYDPEEEKKYTQHPQFKREESLR
IYESHJGMSSPEPKINSYANFRDBVLERIKRLGYNAVQIMAIQEHSYYASFGYHVTNF
FARSHFGTPEDDIKSLLDRAHBLGLLVLMDIVHSSNSTLDGUNGFDOTDTHYFHGG
FAPSSRFGTPEDDIKSLLDRAHBLGLLVLMDIVHSSNSTENDGFFFTCIPVPDGVG
PROGREFGFFTDDANVYYLMLNNDLHGLYPDAVSIGEDVSGMPTFCIPVPDGVG
FDYRLHMANDKWIELLKQSDESWKWGDIVHTLTNKRWLEKCYTYASSHDQALVGDKT
IAFWLWKDMYDFMALDRSTFRIDGCIALHKWIRLVTMGLGGSYLNFMGNEFGHPE
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IAFWLWKDMYDFMALDRSTFRIDGCIALHKWIRLVTMGGGSTLNFMGNEFGHPE
IAFWLWKDMYDFMALDRSTFRIDGCIALHKWIRLVTMGGGSTGOAMQHLEEKY
GFMTSEHQYVSRKHEEDKVIIFERGDLVFVFNFHWSNSFFDYRVGCSKPGKYKVALDS
DDALFGGFSRLDHDVDYFTTEHPHDNRPRSFSWYTPSRTAVVYALTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Triticum aestivum"
/mol type="mRNA"
/cultivar="T.A. Florida"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                 /product="1,4-alpha-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="kernels 21
                                                                                                                                                                                                                                                                                                                                                                                                              'note="branching enzyme"
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Query Match Best Local

Similarity

27.5%; 100.0%;

Score 370; Pred. No.

DB 8; 3.3e-93;

Length 2853;

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                                                                                                                                                                                                                                                         1 (bases 1 to 2970)

McCue, K.F., Hurkman, W.J., Tanaka, C.K. and Anderson, O.D.

Starch Branching Enzymes Sbel and Sbe2 from Wheat (Triticum aestivum cv. Cheyenne): Molecular Characterization, Developm Expression, and Homolog Assignment by Diffferential PCR Plant Mol. Biol. Rep. 20 (2), 191-192 (2002)

2 (bases 1 to 2970)

McCue, K.F. and Anderson, O.D.

Direct Submission

Submitted (11-JUL-2000) United States Department of Agricult Submitted (11-JUL-2000)
                                                                                                                                                                                                                                                                                                                                                                                         Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF286319 2970 bp mRNA Triticum aestivum starch branching enzyme
                                                                                                                                                                                                                                   Agricultural Research Service,
94710-1105, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triticum aestivum (bread wheat)
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                                          /note="glucosyltransferase; alpha-1,4-glucan;
alpha-1,4-glucan-6-glucosyltransferase"
                                                                   /gene="Sbe2"
/EC_number="
                                                                                              /gene="Sbe2"
149. .2620
                                                                                                                                                                                                                  location/Qualifiers
/codon start=1
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                                                                                                                          /tissue_type="endosperm"
l. .2970
                                                                                                                                                               mol_type="mRNA"
cultivar="Cheyenne"
                                                                                                                                                                                          organism="Triticum aestivum"
                                                                                                                                                  db_xref="taxon:4565"
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                                                                     _number="2.4.1.81"
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800 Buchanan Street, Albany, CA
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Best Local (
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961 GAACATCCGCATGACAACAGGCCGCGCTCTTTCTCGGTGTACACTCCGAGCAGAACTGCG
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                                                                          CT--ACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG
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CCCGTGCGCTCAACGTGAACAT
                                     CCCGTGCGCTCAACGTGAAAAT 1342
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Pred. No. 7.9e-91;
0; Mismatches 4
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JAMES AP338432

AP338432

AP338432

Triticum aestivum starch branching enzyme IIa variant mRNA, complete cds.

ESSION

AF338432

AF33843
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PUBMED
REFERENCE
AUTHORS
TITLE
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ACCESSION
VERSION
KEYWORDS
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TASBA2
T.aestivum mRNA for starch branching
Y11282
Y11282.1 GI:1885343
1,4-alpha-glucan branching enzyme; sk
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                                                                                                                                                                                                                                          CT--ACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG 2704
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/product="starch branching enzyme IIa variant"
/product="starch branching enzyme IIa variant"
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/db_xref="starch branching enzyme pahaQpeelQIPEDIEEQTAEVNMTGGT
/translation="mATFAVSCATLGVARPPAhAQPEELQIPEDIEEQTAEVNMTGGT
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ALDYRYSEYRRIRAAIDQHEGGLEAFSRGYEKLGFTRSAEGITYREWAPGAHSAALVG
DFNNNWPHADJMYMTADVGWEIFIPLNNANGSPALPHGSRVKIRNDTPSGVKDSISAWI
KFSVQAPGEIPENGIYYAPPEEEXYVPOHPQFREBLKYIXBSHIGMSSPEPKINSYA
NFRDEVLPRIKRLGYNAVQIMAIQEHSYYASFGYHVTNEFAPSSRFGTEDLKSLIDR
AHELGLIVLMDIVHSHSSNNTLDGLNGFDGTDTHYFHGGPTGHYGEYFGFATDYDAVV
YLMIVNDLIHGLHPDAVSIGFREDGVTSMMYTHHGLQMTPTGNYGEYFGFATDYDAVV
YLMIVNDLIHGLHPDAVSIGFREDGVTSMMYTHHGLQMTPTGRYDEYRIGHDAVDRYIFMILLKQ
SDESWKYAGDIVHTLTNNRWLEKCVTYABSHDQALVGDKTIAFWLMXCMYDFMALDRP
STPRIDRGIALHKWIRLTMRGAGEGYLNFMGNEFGHEBWIDFPRGPCTLFTGKYLEDKV
IIFERGDLYFVUNTHGNGLGGEGYLNFMGNEFGHEBWIDFPRGPCTLFTGKKHEEDKV
IIFERGDLYFVUNTHWSNSFFDYRYGGGERGXKVALDSDDALFGGFSRLDHDVDYFT
TEHPHDNRPRSFSVYTPSRTAVVYALTE"
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/mol_type="mRNA"
/db_xref="taxon:4565"
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Pred. No. 1.5e-90;
0; Mismatches 4;
                                                                                                                                                                       2725
   enzyme; sbe2 gene; starch branching
                                                                            TIRNA
                                                         enzyme
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                                                                                                 al Similarity
375; Conserv
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961 GAACATCCGCATGACAACAGGCCGCGCTCTTTCTCGGGTGTACACTCCGAGCAGAACTGCG 1020
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Triticum aestivum (bread wheat)
Triticum aestivum
Vividiplantae; Strep
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nair,R.B., Baga,M., Scoles,G.J., Kartha,K.K. and Chibbar,R.N. Isolation, characterization and expression analysis of a starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 2970) Chibbar, R.N.
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GAACATCCGCATGACAACAGGCCGCGCTCTTTCTCGGTGTACACTCCGAGCAGAACTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="11.4-alpha-glucan branching enzyme II"
/protein id="CaA72154.1"
/db_xref="03:185344"
/db_xref="03:185344"
/db_xref="GA:P93691"
/db_xref="SpTREMBI:P93691"
/db_xref="SpTREMBI:
                                                                                                                                                 Conservative
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2930. .2935
/gene="sbe2"
2948
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2879. .2884
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151. .2622
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313. .2619
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/EC_number=";
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                                                                                                                                                                                                                                                                                                                                                    'gene="sbe2"
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98.2%;
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Pred. No. 2.2e-90;
0; Mismatches 5
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AF064560
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ar064560 2554 bp mRNA linear PLN 03-NOV-199 mRNA, nuclear gene encoding plastid protein, complete cds. AF064560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sun.C., Sathish,P., Ahlandsberg,S. and Jansson,C. The two genes encoding starch-branching enzymes IIa differentially expressed in barley Plant Physiol. 118 (1), 37-49 (1998)
                                                                                                                                                                                                                                                                                                                                                            Stockholm S-10691, Sweden Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (11-MAY-1998) Stockholm University, Biochemistry,
                                                                                                                                                                                                                                                                                                                                                                                                            Sun, C., Satnish, r
Direct Submission
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QVVPKPGDGQKIYEIDFTLKDFRSHLDYRYSEYKRIRAAIDQHEGGLEVFSRGYEKLG
FTRSAKGITYREMAFGAHSAALVGDFNIWINPINADTMTRDDYGYMEIFLENNADGSPAI
PHGSRVKIRMDTPSGVKDSISAMIKFSVQAPGBIPFNGIYDPBEEEKYVFQHPOPAF
PESLRIYESHIGMSSPEPKINSYANFRDEVLFRIKKLGYNAVQIMAIQBHSYYASFGY
HVTNFFAAPSRRGTPEDLKSLIDRAHELGLLVLMDIVHSHSSNNTLDGLMGFDGTDTH
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                                                                                                                                                                              /gene="sbella"
/EC_number="2.4
                                                                                             /product="starch branching enzyme IIa"
/protein id="AAC69753.1"
/db xref="GI:3822020"
/translation="MAEVNMTGGAAEKLESSEPTQGIAETITDGVTKGVKELVVGEKP
                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                            gene="sbella"
                                                                                                                                                                                                                                                              db_xref="taxon:112509"
chromosome="2"
                                                                                                                                                                                                                                                                                               'mol_type="mRNA"
'cultivar="Bomi"
                                                                                                                                                                                                                                                                                                                            organism="Hordeum vulgare
                                                                                                                                                                               number="2.4.1.18"
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Best Local |
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GLQMTFTGNYGEYFGFATDVDAVVYLMLVNDLIHGLYPDAVSIGEDVSGMPTFCIPVF
DGGVGFDYRLHMAVADKWIELLKQSDESWKWGDIVHTTLTNRRWLEKCYTYAESHDQAL
VGDKTLAF WLMDKDMYDFMALDFFSTFRIDRFALHKWILTWGLGGGEYLNFMGNE
FGHPEWIDF PRGPQTLPTGKYLPGNNNSYDKCRRRFDLGDADFLRYRGNQEFDQAMQH
LEEKYGFMTSSHQYVGRKHEEDKVIIFERGDLVFVFNPHWSNSKDYRVGCSKDGKYK
VALDSDDALFGGFSRLDHDVDYFTTEHPHDNRPRSFSVYTPSRTAVVYALTE"
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sequence.
BT008928
BT008928.1 GI:3212
FLI CDNA.
Triticum aestivum
Triticum aestivum
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Triticum aestivum
                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

1 (bases 1 to 2549)
                                                                                                                                                                                                              Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours a Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
                                                                                                                                                                                                                                                            Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
h 11.8%;
Similarity 90.9%;
69; Conservative
                                                                                                                                                                                                                                                 Direct Submission
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                                                                                    /organism="Triticum aestivum"
/mol type="mRNA"
/db xref="taxon:4565"
/clone="wde1f.pk002.g8:fis"
                                                                                                                                                                           Location/Qualifiers
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Pred. No. 4.5e-63;
0; Mismatches 24;
Score 158.8; DB 8
Pred. No. 2.3e-33;
0; Mismatches 17
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wdelf.
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E.pk002.g8:fis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays subsp. mays (maize)

Zea mays subsp. mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Foales; Poaceae; PACCAD

Clade; Panicoldaee; Andropogoneae; Zea.
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Zea mays subsp. mays cultivar CML333 amylose extender
starch-branching enzyme (ael) gene, exons 19 through 22 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA Location/Qualifiers
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Whitt, S.R., Wilson, I.M., Tenaillon, M.I., Gaut, B.S. and Buckler, E. Genetic diversity and selection in the maize starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
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/gene="ae1"
/number=21
1132 >1292
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                                                                                                                                                                                                                                                                                                                                                                                                            /gene="ae1"
join(<9. .8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
/cultivar="CML333"
                                                                                                                                                                                                                                                 /codon_start=1
/product="amylose extender starch-branching enzyme|
/protein_id="AAP05858.1"
/db_xref="GI:30026553"
                                                                                                                                                                                                                                                                                                                                 join(<9. .86,351.
/gene="ael"
                                                                                                                                                                                                                                                                                                                                                    /product="amylose extender starch-branching enzyme"
join(<9. .86,351. .506,961. .1035,1132. .1215)
                                                                                                                                                                                                                                                                                                                                                                                         gene="ae1"
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                                                                          number=20
                                                                                                                                                                                           DCSHDNRPYSFSVYTPSRTCVVYAPVE
                                                                                          gene="ae1"
                                                                                                                                  number=19
                                                                                                                                                    gene="ae1"
                                                                                                                                                                                                                translation="GDADYLRYHGMQEFDQAMQHLEQKYEFMTSDHQYISRKHEEDKV
VFEKGDLVFVFNFHCNNSYFDYRIGCRKPGVYKVVLDSDAGLFGGFSRIHHAAEHFX
                                                 .1035
>1292
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Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Paccaae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (basss 1 to 1373)
Whitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S. and Buckler, E.S.
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
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Zea mays subsp. mays cultivar A6 amylose extender starch-branching
enzyme (ae1) gene, exons 19 through 22 and partial cds.
AY235395
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/number=22
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ADCSHDNRPYSFSVYTPSRTCVVYAFVE"
  /gene="ae1"
/number=19
                                                                                                                                                                                           Join(<57. .134,401. .556,1010. .1084,1181.
/gene="ae1"
                                                                                                                                                                                                                                                                                                                                                    /organism="Zea mays subsp.
/mol_type="genomic DNA"
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|oin(<57. .134,401. .556,1010. .1084,1181. .1264)
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gene="met"
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83.0%; Pred. No. 6.3e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays subsp. mays (maize)
Zea mays subsp. mays
Eukaryota, viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, viridiplantae, Streptophyta; Embryophyta; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1374)
Whitt,S.R.; Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
                                                                                                                                                                                                                                           Submitted (12-FEB-2003) Genetics, USDA-ARS, North University, 3513 Gardner Hall, Box 7614, Raleigh, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AY235421 1374 bp DNA linear PLN 20-F
Zea mays subsp. mays cultivar TX601 amylose extender
starch-branching enzyme (ael) gene, exons 19 through 22 and
                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1374)
Whitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S. and
                                                                                                                                                                                                                                                                                                                                                                                             22247734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AY235421.1 GI:30026586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGTGATCATCCTCAAAAGAGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTAACTGCAGTTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATA
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/gene="ae1"
/number=20
1010. .1084
/gene="ae1"
/number=21
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/gene="ae1"
/number=22
join(<58. .135,402. .557,1011. .1085,1182. .../gene="ae1"
/codon_start=1
                                                                                                                                                /organism="Zea mays subsp. mays"
/mol type="genomic DNA"
/cultivar="TX601"
/db xref="taxon:4578"
                                                                             join(<58. .135,402. .557,1011. .1085,1182. .>1374)
|gene="ae1"
                                                                                                                gene="ael"
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Pred. No. 6.3e-26;
0; Mismatches 31;
extender starch-branching enzyme"
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                                                                                                                                                                                                                                                                  Carolina State
NC 27695, USA
                                               g enzyme"
.1265)
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AY235405
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AUTHORS
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JOURNAL
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                                                                                                                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.9%;
Best Local Similarity 83.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       571 TT 572
                                                                                                            Direct Submission
Submitted (12-FEB-2003) Genetics, USDA-ARS, North Carolina State Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
                                                                                                                                                                                                                                                                                                                         Zea mays subsp. mays (maize)
Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AY235405 DNA linear PLN 20-APR-2003
Zea mays subsp. mays cultivar D940Y amylose extender
starch-branching enzyme (ael) gene, exons 19 through 22 and partial
                                                                                                                                                                                                                                                                I (Dases 1 to 1382)

Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E. Genetic diversity and selection in the maize starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)
                                                                                                                                                                                            2 (bases 1 to 1382)
Whitt,S.R., Wilson,L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AY235405
AY235405.1 GI:30026554
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1011. .1085
/gene="ae1"
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Ivfekgdlvfvfnfhcnnsyfdyrigcrkpgvykvvldsdaglfggfsrihhaaehft
adcshdnrfysfsvytpsrtcvvyafve"
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       /db_xref="taxon:4578"
                          /organism="Zea mays subsp. mays"
/mol type="genomic DNA"
/cultivar="D940Y"
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/gene="ae1"
                                                                                                    Location/Qualifiers
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/db_xref="GI:30026587"
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 >1382
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Pred. No. 6.3e-26;
0; Mismatches 31;
                                                                                                                                                                                             Tenaillon, M.I.,
                                                                                                                                                                                               Gaut, B.S.
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TITLE
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AY235396.1
                                                                                                   1 (bases 1 to 1393)
Whitt, S.R., Wilson, L.M., Tenaillon, M.I., Gaut, B.S. and Buckler, E. Genetic diversity and selection in the maize starch pathway Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002) 22247734
                                                                                                                                                                                    Zea mays subsp. mays (maize)

Zea mays subsp. mays

Lea mays subsp. mays

Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,

Spermatophyta, Magnoliophyta, Liliopsida, Foales, Poaceae, PACCAD

clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                            AY235396 Inear PLN 20-F
Zea mays subsp. mays cultivar B103 amylose extender
starch-branching enzyme (ae1) gene, exons 19 through 22 and
Direct Submission
Submitted (12-FEB-2003)
                                                2 (bases 1 to 1393)
Whitt, S.R., Wilson, L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTAACTGCAGTTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATA 312
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/gene="ae1"
/number=22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="gdadylryhgmqefdqamqhleqkyefmtsdhqytsrkheedky
Ivfekgdlvfvfnfhcnnsyfdyrigcrkpgvykvvldsdaglfggfsrihhaaehft
adcshdnrfysfsvytpsrtcvvyafve"
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join(<57. .134,402. .557,1011. .1085,1182. .>1382)
/gene="ae1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="amylose extender starch-branching enzyme'
/protein_id="AAP05859.1"
/db_xref="GI:30026555"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="amylose extender starch-branching enzyme"
oin(<57. .134,402. .557,1011. .1085,1182. .1265)
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/number=21
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Pred. No. 6.3e-26;
0; Mismatches 31;
   Genetics,
                                                      Tenaillon, M.I.,
   USDA-ARS,
                                                      Gaut, B.S.
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   North
   Carolina
                                                    and Buckler, E.S
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Best Local
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ilarity 83.0%;
Conservative
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1176. .>1393
/gene="ae1"
/number=22
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1005. .1079
/gene="ae1"
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Ivfekgdlvfvfnfhcmnsyfdyrigcrkfgvykvvldsdaglfggfsrihhaaehft
adcshdnrpysfsvytfsrtcvvyaþve"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays subsp.
/mol_type="genomic DNA"
/cultivar="B103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="amylose extender starch-branching enzyme"
/protein_id="AAP05850.1"
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join(<57. .134,401. .556,1005. .1079,1176.
/gene="ae1"
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join(<57. .134,401. .556,1005. .1079,1176. .1259)
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                                                                                                                         rGACTACCGTATTGGTTGTCGAÁAGCCTGGGGGTGTATAAGGTATGCATCTATC 569
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Pred. No. 6.3e-26;
0; Mismatches 31
                  10:02:30
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 200000000
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Listing first 45 summaries
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1344
1 ttagatatcgtggtatgcaa.....tgcgctcaacgtgaaaatcc 1344
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                         3373863 seqs, 2124099041 residues
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geneseqn2000s:*
geneseqn2001as:*
geneseqn2001bs:*
geneseqn2002s:*
geneseqn2003as:*
geneseqn2003bs:*
geneseqn2003bs:*
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10857.595 Million cell updates/sec
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

WO9914314-A1

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120.6	120.6	120.6	122.4	122.6	122.6	122.6	123.4	123.4	123.4	124	124.2	124.4	125.6	132.4	146	347.6	360	360.6	367.4	370	1344	1344	Score	,
9.0	9.0	9.0	9.1	9.1	9.1	9.1	9.2	9.2	9.2	9.2	9.2	9.3	9.3	9.9	0	25.9	o	26.8	J	27.5	100.0	100.0	Match	Query
2665	2640	636	1267	3039	2968	1036	3015	2655	2304	1087	1120	2307	2307	23449	1085	977	984	2726	979	1119	11475	11473	Length Length	
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AAT69729	AAV70961	ADC08852	ADC08721	ABK15494	AAH78342	AAZ99939	AAV05639	ADA71289	ADC08218	AAZ99940	AAZ99941	ADC07807	AAZ99938	AAZ35393	AAZ99962	AAZ99947	AAZ99946	AAH78337	AAZ99942	ADC08713	AAH78338	AAX34650		
Aat69729 Plasmid p	1960	Corn	Adc08721 Wheat DNA	Wheat			Aav05639 Rice type		8218 Rice		Aaz99941 Nucleotic	-		Maiz			Aaz99946 Nucleotid	_		Adc08713 Wheat DNA	Aah78338 Nucleotid	Aax34650 Starch br	HOLDGIADSAG	

The invention relates to a novel enzyme of starch biosynthetic pathway in a cereal plant, where the enzyme is selected from starch branching enzyme (SBB) I, starch soluble synthase (SSS) I, and debranching enzyme (DBB), with the proviso that the enzyme is not SSS I of rice, or SBE I of

Claim 8; Page 75-81; 171pp; English.

New isolated cereal plant enzyme genes used for, antisense sequences of granule bound synthase.

e.g. expression

WPI; 1999-229525/19.

Li Z,

Morell M,

Rahman S;

(CSIR) COMMONWEALTH SCI & IND RES ORG.
(AUSU) UNIV AUSTRALLAN MAT.
(GCODD-) GOODMAN FIBELDER LITD.
(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

12-SEP-1997; 20-MAR-1998; 11-SEP-1998; 25-MAR-1999.

97AU-00009108. 98AU-00002509. 98WO-AU000743.

ALIGNMENTS

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RESULT 1
AAX34650
ID AAX34650
AAX4650
AAX34650
AAX3460
AAX34650
AAX3460
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Query Match
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GCTTGATCATGATGTCGACTACTTCACAACCGTAAGTCTGGGCTCAAGCGTCACTTGACT
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Pred. No. 0;
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Nucleotide sequence of a starch branching enzyme designated

starch branching biosynthetic path enzyme; ne; BEIIb; SBE;
amylopectin; F BEIIb; F2;

Aegilops tauschii

WO200162934-A1

21-FEB-2001; 2001WO-AU000175

21-FEB-2000; 2000AU-00005742

(CSIR) COMMONWEALTH SCI & IND RES (GOOD-) GOODMAN FIELDER LTD. (LIMA-) GRP LIMAGRAIN PACIFIC PTY) ORG

LTD.

Rahman S;

WPI; 2001-570635/64.

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> Nucleic acids ealtering the anand barley. acids encoding wheat starch branching the amylose and amylopectin content of g enzyme IIb, useful of cereal plants, e. wheat

Example 1; Fig 2 103pp; English

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Matches 1344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11475 BP; 3093 A; 2259 C; 2423 G; 3689 T; 0 U; 11 Other;
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tomato; banana; canola; cotton; pea
wheat; rice; protein; oil; starch;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved
                                                                                                                                  Zhu T, Chi
Glazebrook
                                                                                                                                                                                                                                          22-JUN-2001; 2001US-0300112P
26-SEP-2001; 2001US-0325277P
20-DEC-2001; 2001US-0342327P
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                                                                                                                                Cheng
                                                                                                                                                                                                    SYNGENTA PARTICIPATIONS
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                                                                                                                              y W, Briggs
Katagiri F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                         ຸສຸດ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carbohydrate; plant grain; grain filling;
otton; peanut; sorghum; tobacco; sugarbeet;
                                                                                                                                  Kreps
                                                                                                                                Cooper E
Kreps J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
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                                                                                                                                     Moughamer Ricke D;
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11091 960

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                                                                                                               Wheat; starch branching enzyme II; SBEII; SBEII-2; gelatinisation onset; transgenic plant; foodstuff;
                                                                                  Triticum aestivum
                                                                                                                                                                 Nucleotide sequence
                                                                                                                                                                                                 25-JUL-2000
                                                                                                                                                                                                                                                                  AAZ99942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention, in the area of plant biotechnology, relates to novel
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                                                                                                                                                                                                                                                                  standard;
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                                                                                                                                                                                                                                                                  DNA;
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                                                                                                                                                                  of starch
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100.0%;
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Pred. No.
                                                                                                                                                                 branching enzyme
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                                                                                                                                                                    II clone
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                                                                                                               starch; SBEII-1;
bakery product;
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     RESULT 5
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ID AAH7
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26-NOV-2001

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standard; cDNA; 2726

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated starch gelatinization onset and/or peak temperature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 124; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goldsbrough A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                          CCCGTGCGCT
                                                                                  CTGAACCCTCCTCCTATCTTGCACATTCCCCGGTTGTTTTTGTACATATAACTAATAATTG
                                                                                                                                                    CGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGGAGCAGATGGATAG
                                                                                                                                                                                                                                                 CTCCAGAGAGCTCGTGGATCGTGAGCGAAGCGACGGCAACGGCGCGAGGCTGCTCCAAG
                                                                                                                                                                                                                                                                            CTCCAGAGAGCTCGTGGATCGTGAGCGAAGCGACGGCCAACGGCGCGAGGCTGCTCCAAG
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CCCGTGCGCT 927
                                                            CTGAACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                           1330
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 367.4; DB 3;
Pred. No. 5.8e-105;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 T; 0 U; 1 Other;
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Nucleotide seguence

of wheat starch branching

enzyme 9

(BEIIa)

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Query Match
Best Local S
Matches 375
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starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes wheat starch branching enzyme 9, designated BEIIa. The specification describes BEIIb BEIIb is a type II starch branching enzyme (SBE). The BEIIb nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding wheat starch branching altering the amylose and amylopectin content of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2726
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(GOOD-)
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2705
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375; Conserv
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GOODMAN FIELDER LTD.
GRP LIMAGRAIN PACIFIC PTY I
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                                                                                                                                                                                 CGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGGAGCAGATGGATAG
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                                                                                                                                                                                                                                                                                                                                                                                                 GTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCTGCTTGTTACAAGGCAAAGAGAGAA
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                                   CCCGTGCGCTCAACGTGAAAA 1341
                                                                                                               CTGAACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG
                                                                                                                                                                                                                                    CGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGCAGATGGATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      726 A; 564 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.8%;
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amylopectin; amylose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 360.6; DB 5;
Pred. No. 1.5e-102;
0; Mismatches 4;
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2725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ი</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      735 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g enzyme IIb, useful for of cereal plants, e.g. wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a clone of wheat starch branching enzyme II (SBEII), which is part of a novel subclass of known SBEII genes, designated SBEII-1. The specification also describes subclass SBEII-2 sequences. The SBEII-1 genes are thought to have similar functional properties to the maize SBEIIb gene. Starch branching enzymes catalyse the formation of the alpha-1,6 linkages, creating branch points in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage followed by reattachment of the released alpha-1,4-glucan chain to the same or another glucosyl chain. SBEII polypeptides can be used to alter the characteristics of a plant, in particular to alter starch so that it has an elevated gelattinisation onset and/or peak temperature. Starch obtained from transgenic plants is useful in the preparation or processing a foodstuff, particularly bakery products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated stargelatinization onset and/or peak temperature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gelatinisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 984 BP; 268 A; 212 C; 250 G; 254 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goldsbrough A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200015810-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PLAN-) PLANT BREEDING INT CAMBRIDGE
                    1201
                                                                                                                                                                                                                                         1081
                                                                                                                                                                                                                                                                                                                                                    1021
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                                                                                                                                                                                     678
                                                                                                                                                                                                                                                                                                618
                                                                                                                                                                                                                                                                                                                                                                                                                                                      961 GAACATCCGCATGACAACAGGCCGCGCTCTTTCTCGGTGTACACTCCCGAGCAGAACTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375;
                                                                        738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          starch branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                           GTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCGGCTTGTTACAAGGCAAAGAGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                           GAACATCCGCATGACAACAGGCCGCGCTCTTTCTCGGTGTACACTCCGAGCAGAACTGCG
CGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGGAGCAGATGGATAG
                                                                                                                                                                                     CTCCAGAGAGCTCGTGGATCGTGAGCGAAGCGACGGGCAACGGCGCGAGGCTGCTCTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 168; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.8%;
98.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 360; DB
; Pred. No. 1.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plant;
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foodstuff;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .3e-102;
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bakery p
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           Query Match
Best Local :
Matches
                                                                           The present sequence represents a clone of wheat starch branching enzyme II (SBEII), which is part of a novel subclass of known SBEII genes, designated SBEII-1. The specification also describes subclass SBEII-2 sequences. The SBEII-1 genes are thought to have similar functional properties to the maize SBEIIb gene. Starch branching enzymes catalyse the formation of the alpha-1,6 linkages, creating branch points in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage followed by reattachment of the released alpha-1,4-glucan chain to the same or another glucosyl chain. SBEII polypeptides can be used to alter the characteristics of a plant, in particular to alter starch so that it has an elevated gelatinisation onset and/or peak temporature. Starch obtained from transgenic plants is useful in the preparation or processing a foodstuff, particularly bakery products
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gelatinisation
                                                                                                                                                                                                                                                                            Disclosure; Page 168-169; 197pp; English.
                                                                                                                                                                                                                                                                                                      gelatinization
                                                                                                                                                                                                                                                                                                                   DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated starch
                                                                                                                                                                                                                                                                                                                                                                                                      Goldsbrough A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200015810-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of starch branching enzyme II
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (PLAN-)
                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       starch branching enzyme II; SBEII; SBEII-1;
nisation onset; transgenic plant; foodstuff;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PLANT
              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCGTGCGCTCAACGTGAACAT 937
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                                                     977 BP; 270 A; 200 C; 245 G; 262 T; 0 U; 0 Other;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                   BREEDING INT CAMBRIDGE
                                                                                                                                                                                                                                                                                                         onset
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "starch branching
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry!
                                                                                                                                                                                                                                                                                                        and/or peak temperature.
             25.9%;
96.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    977
0,
Score 347.6; DB 3;
Pred. No. 1.1e-98;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                   LID
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                           Length
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GAACATCCGCATGACAACAGGCCGCGCTCTTTCTCGGTGTACACTCCCGAGCAGAACTGCG

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RAESULT 8
AAZ9962
ID AAZ9
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The present sequence represents the consensus sequence of wheat starch branching enzyme II (SBSII). The specification describes novel subclasses of SBSII designated SBSII-1 and SBSII-2. The SBSII-1 genes are thought to have similar functional properties to the maize SBSIIb gene. Starch branching enzymes catalyse the formation of the alpha-1, 6 linkages, creating branch points in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage followed by reattachment of the released alpha-1,4-glucan chain to the same or another glucosyl chain. SBSII polypeptides can be used to alter the characteristics of a plant, in particular to alter starch so that it has an elevated gelatinisation onset and/or peak temperature. Starch obtained from transgenic plants is useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated starch
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                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 187; 197pp; English.
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/transl_except= (pos: 2091.
/transl_except= (pos: 2096.
/transl_except= (pos: 2196.
/transl_except= (pos: 2114.
/transl_except= (pos: 2114.
/transl_except= (pos: 2174.
/transl_except= (pos: 2174.
/transl_except= (pos: 2174.
/transl_except= (pos: 2306.
/t
                                            98EP-00307337
                                                                                                                     99WO-GB003011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product= "starch branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 23449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6. .2098
4. .2116
7. .2179
8. .2170
8. .2170
9. .2191
9. .2291
7. .2269
9. .2272
6. .2307
                                                                                                                                                                                                                                                                                                                                                                                                  amino acid; the sequence codons, but no termination
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.2053,
.2092,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aa: Xaa)
aaa: Xaa)
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intron

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misc_feature

polyA_signal

Guiltinan MJ,

Kim K;

(UYPE-) UNIV

PENNSYLVANIA STATE

12-JUN-1998; 12-JUN-1998;

99WO-US013266. 98US-0089049P. 98US-0089050P. WO9964562-A2 16-DEC-1999.

11-JUN-1999;

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13080. .13208 // number = 14 // number = 14 // number = 14 // 16260. .16363 // number = 15 // 16364. .17235 // 17236. .17380 // number = 16 // 17381. .17381 // 17381. .17381 // 17381. .17381 // 17381. .17381 // 17381. .17381 // 17381. .17381 // 17381. .17381 // 17381. .17381 // 17381. .17381 // 17381. .17381 // 17381. .17381 // 17381. .17381 // 17381. .17381 // 17381. .17381 // 17381. .17381 // 17381. .1839 // number = 19 // 18310. .18230 // 18310. .18230 // 18310. .1834 // 1835. .18458 // 1835. .19404 // 1835. .19404 // 1835. .19404 // 1836. .19575 // 19480. .19575 // 19480. .19575 // 19481. .19596 // 19481. .19659 // 19481. .19659 // 19481. .19849 // 19481. .19849 // 19481. .19849 // 19481. .19849

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Best Local S
Matches 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a wheat starch branching enzyme II (SBEII) of a novel subclass of known SBEII genes, designated SBEII-1. The SBEII-1 genes are thought to have similar functional properties to the maize SBEIIb gene. Starch branching enzymes catalyse the formation of the alpha -1,6 linkages, creating branch points in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage followed by reattachment of the released alpha-1,4-glucan chain to the same or another glucosyl chain. SBEII polypeptides can be used to alter the characteristics of a plant, in particular to alter starch so that it has an elevated gelatinisation onset and/or peak temperature. Starch obtained from transgenic plants is useful in the preparation or processing a foodstuff, particularly bakery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated starch gelatinization onset and/or peak temperature.
          22-JUN-2001; 2001US-0300112P.
26-SEP-2001; 2001US-0325277P.
20-DEC-2001; 2001US-0342327P.
                                                                                                                     Oryza
                                                                                                                                        gene;
                                                                                                                                                    plant biotechnology; carbohydrate synthesis; carbohydrate metabolism; carbohydrate degradation; carbohydrate; plant grain; grain filling; c tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet; wheat; rice; protein; oil; starch; fibre; moisture content; cereal gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goldsbrough A,
                                                     21-JUN-2002;
                                                                           03-JAN-2003
                                                                                               WO2003000905-A2
                                                                                                                                                                                                                              18-DEC-2003
                                                                                                                                                                                                                                                    ADC07807;
                                                                                                                                                                                                                                                                         ADC07807
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                                                                                                                                          dB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                     CTCAAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                               TTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2307
                                                                                                                                                                                                                                                                                                                               TACCGGGTTGGCTGTTTAAAGCCTGGGAAGTACAAGGTTGTCTT
                                                                                                                                                                                                                                                                                                                                             TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTT
                                                                                                                                                                                                                                                                                                                                                                        TTTGAAAAAGGGGACTTGGTATTTGTGTTCAACTTCCACTGGAGTAATAGCTATTTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                   TTTATGACATCAGACCACCAGTACGTATCTCGGAAACATGAGGAAGATAAGGTGATCGTG 1567
                                                                                                                                        plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                              (first entry)
                                                      2002WO-IB002450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BREEDING
                                                                                                                                                                                                        Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        674 A; 440 C; 544 G;
                                                                                                                                                                                                                                                                         DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
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                                                                                                                                                                                                         related
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 125.6; DB 3;
Pred. No. 2.9e-28;
0; Mismatches 24;
                                                                                                                                                                                                                                                                            86
                                                                                                                                                                                                         ö
                                                                                                                                                                                                         grain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        635 T; 0 U; 14 Other;
                                                                                                                                                                                                         filling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                   427
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                                                                                                                                                    cereal grain;
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                                                                                                                                                                                                                                                                                                                                                                                               383
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RESULT 12
AAZ99941
ID AAZ999
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AC AAZ99
XX
AC AAZ99
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VICTOR Nucle
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Wheat
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Wheat
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Wheat
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Who Blat
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WO200
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PD WO200
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Best Local :
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                     10-SEP-1998;
                                           09-SEP-1999;
                                                                                                                                                                                     25-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                   137;
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This invention, in the area of plant biotechnology, relates to novel polymucleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence encoding a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved nutritional properties.
                                                                                                                                                                                                                                         Wheat; starch l gelatinisation
                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of starch branching enzyme II clone B10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ99941 standard; DNA; 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; SEQ ID NO 73; 130pp; English.
                                                                                                                                    WO200015810-A1
                                                                                                                                                                                         Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2307 BP; 608 A; 465 C; 620 G;
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Similarity 86.7%;
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ook J, Katagiri E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTCGAGAGAGATTTGGTATTCGTGTTCAACTTCCACTGGAGTAATAGCTATTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTCAAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGA
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                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                         branching enzyme II; SBEII; SBEII-1; starch;
n onset; transgenic plant; foodstuff; bakery !
                              99WO-GB003011.
                                                                                                                                                                                                                                                                                                                                                                             entry
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Kreps J, Provart N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 124.4;
Pred. No. 7e-2
0; Mismatches
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Ricke D;
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                                                                                                                                                                                                                                              product;
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(PLAN-) PLANT BREEDING INT CAMBRIDGE LTD

98EP-00307337.

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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a clone of wheat starch branching enzyme II (SBEII), which is part of a novel subclass of known SBEII genes, designated SBEII-1, subclass B. The specification also describes subclass SBEII-2 sequences. The SBEII-1 genes are thought to have similar functional properties to the maize SBEII genes. Starch branching enzymes catalyse the formation of the alpha-1,6 linkages, creating branch points in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage followed by reattachment of the released alpha-1,4-glucan chain to the same or another glucosyl chain. SBEII polypeptides can be used to alter the characteristics of a plant, in particular to alter starch so that it has an elevated gelatinisation onset and/or peak temperature. Starch obtained from transgenic plants is useful in the preparation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated starch gelatinization onset and/or peak temperature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goldsbrough A,
                                                                                                                                                                                            Wheat; starch branching enzyme II; SBEII; SBEII-1;
gelatinisation onset; transgenic plant; foodstuff;
                                                                                                                                                                                                                                               Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1120 BP; 338 A; 208 C; 252 G; 308 T; 0 U; 14 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   processing a foodstuff, particularly bakery products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 123-124; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-271446/23
                                                                                                                                                                  Triticum aestivum
                                                                                                                                                                                                                                                                            25-JUL-2000
                                                                                                                                                                                                                                                                                                           AAZ99940
                                                                                                                                                                                                                                                                                                                                        AAZ99940 standard; DNA; 1087
                                                                       09-SEP-1999;
                                                                                                      23-MAR-2000.
                                                                                                                                   WC200015810-A1.
         (PLAN-) PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                     505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCAAAAGAGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTTGAC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTATGACATCAGACCACCAGTACGTTTCTCGGAAACATGAGGAAGATAAGGTGATCGTG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGGAAGATAAGGTGATCATC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTTGCCTTTTCATTGTCCA 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTGAAAAAGGGGACTTGGTATTTGTGTTCAACTTCCACTGGAGTAGTAGCTATTTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACCGGGTCGGCTGTTTAAAGCCTGGGAAGTACAAGGTGGTCTTAGACTCGGACGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                            (first
           BREEDING INT CAMBRIDGE
                                                                                                                                                                                                                                                                                                                                                                                                                     509
                                                                                                                                                                                                                                                                                                                                                                                                                                                  448
                                          98EP-00307337.
                                                                         99WO-GB003011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.2%;
                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                             of starch branching enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 124.2; DB 3;
Pred. No. 5.2e-28;
0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                            ₽P
             CLT
                                                                                                                                                                                                                                               II clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1120;
                                                                                                                                                                                                starch; SBEII-2;
bakery product;
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RESULT 14
ADCO88
ID ADCO88
XX ADCO88
AC ADCO8
XX 18-DE
XX 18-DE
XX Plant
KW Carbo
KW Carbo
KW Wheat
KW Wener
XX OFYZZZ
XX WO200
XX W0200
XX 22-JI
XX 22-JI
XX 22-JI
XX 22-JI
PR 26-SI
PR 26-SI
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PR 26-SI
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a clone of wheat starch branching enzyme II (SBEII), which is part of a novel subclass of known SBEII genes, designated SBEII-1, subclass C. The specification also describes subclass SBEII-2 sequences. The SBEII-1 genes are thought to have similar functional properties to the maize SBEII gene. Starch branching enzymes catalyse the formation of the alpha-1, 6 linkages, creating branch points in the growing starch molecule, via hydrolysis of an alpha-1, 4 linkage followed by reatrachment of the released alpha-1,4-glucan chain to the same or another glucosyl chain. SBEII polypeptides can be used to alter the characteristics of a plant, in particular to alter starch so that it has an elevated gelatinisation onset and/or peak temperature. Starch obtained from transgenic plants is useful in the preparation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated starch gelatinization onset and/or peak temperature.
                                                                                                                                                                                                                                                                                                                  plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1087 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                    Oryza sativa
                                                                                                                                                                                                                                                    gene;
                                                                                                                                                                                                                                                                                    carbohydrate degradation; carboh
tomato; banana; canola; cotton;
                                                                                                                                                                                                                                                                                                                                                         Rice
                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC08218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goldsbrough A,
                                                                                                                                                    03-JAN-2003.
                                                                                                                                                                                    WO2003000905-A2
                                                                                                                                                                                                                                                                    wheat; rice; protein; oil; starch; fibre; moisture content;
                                                                                                                   21-JUN-2002; 2002WO-IB002450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-271446/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139;
                                                                                                                                                                                                                                                                                                                                                        DNA sequence Seq ID523 related to grain filling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264
                                                                                                                                                                                                                                                    ds; plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTT 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTGAAAAAGGGGACTTGGTATTTGTGTTCAACTTCCACTGGAGTAATAGCTATTTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCAAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTATGACATCAGACCACCAGTACGTATCTCGGAAACATGAGGAAGATAAGGTGATCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCATC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACCGGGTTGGCTGTTTAAAGCCTGGGAAGTACAAGGTTGTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 A; 214 C; 235 G; 296 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2304
                                                                                                                                                                                                                                                                                        carbohydrate; plant grain, grain filling;
otton; peanut; sorghum; tobacco; sugarbeet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 124; DB 3;
Pred. No. 5.9e-28;
0; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1087;
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22-JUN-2001; 2001US-0300112P. 26-SEP-2001; 2001US-0325277P. 20-DEC-2001; 2001US-0342327P.

(SYGN)

SYNGENTA

PARTICIPATIONS

Η.

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RESULT 15
ADA71289
ID ADA71
XX ADA71
XX ADA71
XX ADA71
XX P1-NO
DE Rice
XX P1-NO
CO OTYZA
XX OTYZA
XX OTYZA
XX OTYZA
XX D1-JI
XX 22-JI
XX X 22-JI
XX Chang
PI Chang
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention, in the area of plant biotechnology, relates to novel polynucleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence encoding a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved nutritional properties.
                                                                                                                                                                                     Oryza
                                                                                                                                                                                                                                                               Rice gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2304 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhu T, Cheng
Glazebrook J,
                                                           22-JUN-2001; 2001WO-IB001105
                                                                                                                          03-JAN-2003
                                                                                                                                                       WO2003000898-A1
                                                                                                                                                                                                                  gene,
                                                                                                                                                                                                                                  Plant; bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                                                               20-NOV-2003
                                                                                                                                                                                                                                                                                                                              ADA71289
                                                                                                                                                                                                                                                                                                                                                           ADA71289 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     was obtained in electronic format direct
ftp.wipo.int/pub/publishedpct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                            22-JUN-2001; 2001WO-IB001105
                                (SYGN ) SYNGENTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCAAAAGAGAGTTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCGAGAGAGAGATTTGGTATTCGTGTTCAACTTCCACTGGAGTAATAGCTATTTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCATGACATCTGAGCACCAGTATATATCGCGCAAACACGAGGAGGATAAGGTGATCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                         TATCGCGTCGGTTGTTTAAAGCCTGGAAAGTACAAGATTGTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 523; 130pp; English.
                                                                                                                                                                                                                                                                SEQ ID 4612.
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Katagiri F
                                                                                                                                                                                                                                                                                              (first
                                PARTICIPATIONS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610 A; 457 C;
                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cooper B,
Kreps J, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 123.4; 1
Pred. No. 1.4e.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9;
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Cooper B,

Glazebrook

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Goff SA,

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Best Local :
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                                                                                                                                                                                                                                                                                                       The present invention relates to a method (MI) for identifying genes involved in plant resistance or response to pathogenic infection. MI comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                          Sequence 2655 BP; 714 A; 529 C; 680 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Katagiri F,
2458
                                                                   2398
                                                                                                  324
                                                                                                                                                                                                        139;
                                                                                                                                                                                                                      9.2%;
Similarity 84.2%;
                                                                                                    CTCAAAAGAGAAGTTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGAC
                                                                   TTCGAGAGAGAGATTTGGTATTCGTGTTCAACTTCCACTGGAGTAATAGCTATTTTGAC
TATCGCGTCGGTTGTTTAAAGCCTGGAAAGTACAAGATTGTGTTG
                                TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTTG
                                                                                                                                      TTCATGACATCTGAGCACCAGTATATATCGCGCAAACACGAGGAGGATAAGGTGATCATC
                                                                                                                                                                      TTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCATC
                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID NO 4612; 899pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tao Y,
                                                                                                                                                                                                    Score 123.4; DB 7
Pred. No. 1.6e-27;
0; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whitham
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                                                                                                                                                                                                                                                                            732 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xie
                                                                                                                                                                                                                                            DB 7;
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                                   428
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Search completed: April 10, Job time : 528.86 secs 2004, 04:00:09

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Result
No.
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Maximum DB seq
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Perfect score:
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125.6
120.6
120.7
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                                                                                                                                                                                                                    No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                               9<u>1</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length: 0
length: 2000000000
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1344
1 ttagatatcgtggtatgcaa....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_NA:*

1: /ggn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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(without alignments)
7804.525 Million cei
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Maximum Match 100%
Listing first 45 summaries
   ttagatatcgtggtatgcaa.....tgcgctcaacgtgaaaatcc 1344
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   Length
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US-09-257-894-1
US-09-911-145A-14
US-09-911-145A-14
US-09-658-499-1
US-09-658-499-1
US-09-658-499-1
US-09-257-894-19
US-09-257-894-12
US-09-257-894-12
US-08-104-158-1
US-09-257-894-2
US-08-104-158-1
US-09-257-894-9
US-09-257-894-9
US-09-257-894-8
US-09-257-894-8
US-09-257-894-8
US-09-257-894-8
US-09-257-894-8
US-09-251-976-2813
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        CTGAACCCTCCTCCTATCTTGCACATTCCCCGGTTGTTTTTGTACATAAACTAATAATTG
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ALIGNMENTS

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LENGTH: 2853
; TYPE: DNA
; ORGANISM: Triticum aestivum
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (313)..(2499)
; OTHER INFORMATION: BRANCHING ENZYME
US-09-609-040-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09609040

Patent No. 6570066

GENERAL INFORMATION:

FILE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRATITILE OF INVENTION: CONCENTRATION AND COMPOSITION IN PLANTS

FILE REFERENCE: 514413-3515.1

CURRENT APPLICATION NUMBER: US/09/609,040

CURRENT FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: PCT/EP92/00302

PRIOR FILING DATE: 1992-02-11

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                               2419 GAACATCCGCATGACAACAGGCCGCGCTCTTTCTCGGTGTACACTCCGAGCAGAACTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                              961 GAACATCCGCATGACAACAGGCCGCGCTCTTTCTCGGTGTACACTCCGAGCAGAACTGCG
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                                                                                                                        CGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGGAGCAGATGGATAG
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                                                                                                                                                                                          CTCCAGAGAGCTCGTGGATCGTGAGCGAAGCGACGGGCAACGGCGCGAGGCTGCTCCAAG
                                                                                                                                                                                                                                                                                                GTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCGCTTGTTACAAGGCAAAGAGAGAA
                                       GIAGCITGITGGIGAGCGCICGAAAGAAAAIGGACGGGCCIGGGIGITITGITGITGCIGCA 1260
                                                                                         CGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGGAGCAGATGGATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.5%; Score 370; DB 4; Le
100.0%; Pred. No. 8.6e-110;
tive 0; Mismatches 0;
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APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified Polysaccarides
FILE REFERENCE: 35718/206348
CURRENT APPLICATION NUMBER: US/09/731,166
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
PRIOR FILING DATE: 1999-12-06
                                                                                                                                                                                                                                   Sequence 1, Application US/09257894 Patent No. 6376749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Sin
Matches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09731166 Patent No. 6639126
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SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (2)...(2446)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: (0)...(0) CTHER INFORMATION: SBEIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Genbank Accession No. 6639126 U65948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 2446
                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                APPLICANT: Klein,
APPLICANT: Hubbard
APPLICANT: Lightn
                                                                                                                                                                                              APPLICANT:
                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                         2298
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      Okra...

f: Broglie, Kata...

T: Klein, Theodore M.

T: Klein, Theodore M.

T: Hubbard, Natalie L.

NT: Lightner, Jonathan E.

NT: Lightner, Jonathan E.

FINVENTION: No. 6376749el Starches via Modification of INVENTION: Expression of Starch Biosynthesis

TAMFENTION: Enzyme Genes

TAMFENTION: Signal Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGAACCCTCCTACCTACCTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG
                                                                                                                                                                                                                                                                                                                                                         GCCTTTTC 2305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTTGAGAGAGGAGATTTGGTCTTCGTGTTCAACTTCCACTGGAGCAATAGCTATTTTG
1007 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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79.3%;
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Pred. No. 3.5e-30;
0; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                        GTACAAGATCGTTTTAGATTCTGACGATG 2297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
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Sequence 11, Application US/09731166

Retent No. 6639126

GENERAL INFORMATION:

APPLICANT: Sewalt, Vincent J. H.

APPLICANT: Singletary, George W.

TITLE OF INVENTION: Production of Modified Polysaccarides

FILE REFERENCE: 35718/206348

CURRENT APPLICATION NUMBER: US/09/731,166

CURRENT FILING DATE: 2000-12-06

PRIOR APPLICATION NUMBER: 60169,993

PRIOR FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 2720
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; LOCATION:
US-09-257-894-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.03
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
FILING DATE: JUNE 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: JUNE 10, 19
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 302-773-0164
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Pred. No. 1.6e-28;
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ORGANISM: Zea mays FEATURE: NAME/KEY: misc_feature

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RESULT 5
US-08-941-445A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 138;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Keeling, Peter
APPLICANT: Gean, Hanping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (0)...(0)
OTHER INFORMATION: SBEIIb
OTHER INFORMATION: Genbank Accession No. 6639126 AF072725
NAME/KEY: CDS
LOCATION: (101)...(2500)
                                                                                                                                                                                                                                                                                                      FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-9
TELECOMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                       TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2725 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                      ORIGINAL SOURCE
                                                                                                                     MOLECULE TYPE: mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 5370 |
CITY: Boulder
                                                                                                                                                                                                                                                                TELEPHONE: (303) 499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
                                    NAME/KEY:
                                                                                 ORGANISM:
                                                                                                                                                                TOPOLOGY:
                     OCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 AGTTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 9.0%;
Similarity 82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTTG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTCATGACATCTGATCACCAGTATATTTCCCGGAAACATGAGGAGGAGATAAGGTGATTG 2243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTACCGTATTGGTTGTCGAAAGCCTGGGGTGTATAAGGTGGTCTTG 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTCGAAAAGGGAGATTTGGTATTTGTGTTCAACTTCCACTGCAACAACAGCTATTTTG
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                                                                                                                                                                                                                       2725 base pairs
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                     sig_peptide
91..264
                                                                                                                                                                not relevant
                                                                                 Zea mays
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Pred. No. 1.6e-28;
                                                                                                                                                                                                                                                                                                                                                   89-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Class-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
ITILE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
CURRENT APPLICATION UNMBER: US/09/087,2778
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION UNMBER: PCT/SE96/01558
EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER APPLICATION UNMBER: SE 9504272-7
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LOCATION:
US-08-941-445A-14
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Best Local Similarity 82.6%;
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3074
TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
FEATURE:
NAME/KEY: misc feature
LOCATION: (285)..(287)
OTHER INFORMATION: Amino acid -16 is Xaa wherein
OTHER INFORMATION: or Phe.
                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: CDS
LOCATION: (189)..(2825)
                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Unknown OTHER INFORMATION: (branching enzyme II) f OTHER INFORMATION: (potato)
                                                                                                    NAME/KEY: misc_feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897
OTHER INFORMATION: n wherein n = A, C, G or T.
                                                                                                                                                                                                      NAME/KEY: mat_peptide
LOCATION: (333)..(2825)
                                                                                                                                                                                                                                                                NAME/KEY: sig_peptide
LOCATION: (189)..(332)
                                                                                                                                                                                       FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2174 AATTCATGACATCTGATCACCAGTATATTTCCCCGGAAACATGAGGAGGATAAGGTGATTG 2233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2294 ACTACCGTATTGGTTGTCGAAAGCCTGGGGTGTATAAGGTGGTCTTG 2340
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265..2487
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Pred. No. 1.6e-28;
0; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                   i Organism:beII gene
from Solanum tuberosum
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                         Xaa
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                                                                                                                             PRIOR APPLICATION NUMBER: SE 9504272-7
PRIOR FILING DATE: 1995-11-29
PRIOR APPLICATION NUMBER: SE 9601506-0
PRIOR FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATI
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LOCATION: (2154)..(2156)
OTHER INFORMATION: Amino acid
-09-087-277-1
                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/658,499
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 09/087,277
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: PCT/SE96/01558
PRIOR FILING DATE: 1996-11-28
DEFICE RELIVED DATE: 1996-11-28
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: RASK, LAZE
TITLE OF INVENTION: STARCH BRANCHING ENZYME
FILE REFERENCE: 003300-486
FILE REFERENCE: US/09/658,499
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LARSSON, APPLICANT: LARSSON,
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LOCATION: (1896)..(1898)
OTHER INFORMATION: Amino acid
OTHER INFORMATION: or Phe.
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NAME/KEY: misc_feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                        ORGANISM: Unknown FEATURE:
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                                                                                                                ENGTH: 3074
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Local Similarity 67.9%;
les 127; Conservative
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RASK, Lars
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LARSSON, Clas-Tomas
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Description of Unknown Organism:beII gene (branching enzyme II) from Solanum tuberosum (potato)
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Pred. No. 7.8e-19;
0; Mismatches 60
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US-09-731-166-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
APPLICANT: George W.
APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simi
Matches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/09731166 Patent No. 6639126
                                                                                                                                                                                                                                          SEQ ID NO 13
                                                                                                                                                                                                                                                   FILE REFERENCE: 35718/206348
CURRENT APPLICATION NUMBER: US/09/731,166
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.
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LOCATION: (1896)..(1896)
OTHER INFORMATION: Amino acid 522 is
OTHER INFORMATION: or Phe.
NAME/KEY: misc_feature
LOCATION: (2154)..(2156)
OTHER INFORMATION: Amino acid 608 is
                                               ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
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OTHER INFORMATION: Amino
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OTHER INFORMATION: n wherein n = A,

NAME/KEY: misc feature

LOCATION: (285) . (287)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
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LOCATION: (333)..(282)
                         DOTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (1428)..(1430)
THER INFORMATION: Amino acid
NAME/KEY: CDS
                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2509
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                                                                                                                                                                                                          2470
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(189)..(332)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACTTTT 2635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCCTT 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTCACTGGACAAAAAGCTATTCAG
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                            Genbank Accession
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O; Mismatches
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7.8e-19;
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                               6639126 217959
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; LOCATION: (2)...(2470) US-09-731-166-13

Query Match 4.3%; Best Local Similarity 56.9%; Matches 107; Conservative

Score 58.4; DB 4; Pred. No. 2.8e-08; 0; Mismatches 81;

Length 2470;

Indels

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Gaps

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360
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                                                                  US-09-257-894-24
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Matches 107;
              Query Match
Best Local Similarity
                                                                                                                                                                          TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091
PILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,11
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Version 7.0%
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
                                                                                     STRANDEDNESS:
TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification
TITLE OF INVENTION: Expression of Starch Biosynthesis
                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 100.
CTTY: Wilmington
CTTY: Colonia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320 ATCCCAAGAAACTTACGAGGGCTACAAAGTGGGATGCGATTTGCCTGGGAAATACAGAG
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                                                                                                                                                           2565 base pairs
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1007 Market Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Broglie, Kare.
Klein, Theodore M.
                                                                                                                                                                                                               302-773-0164
                                                                                                         linear
              4.3%;
56.9%;
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Score 58.4; DB 4;
Pred. No. 2.9e-08;
0; Mismatches 81;
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0; Mismatches 81; Indels
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                                 Length 2565;
   Indels
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                                                                                                                                                                                                                                                                                                            TELEPHONE: (303) 499-808
TELEPAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
                                                                                                                                                                                                             TOPOLOGY: not MOLECULE TYPE: r
HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/941,445;
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA: 80
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Keeling, Peter
APPLICANT: Guan, Hamping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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                                                                                                                               FEATURE:
                                            NAME/KEY:
LOCATION:
                                                                                              NAME/KEY:
                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Winner, Ellen P
REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                               ORGANISM:
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                                                                                                                                                OCATION:
                                                                                                                                                                                                                                                                             TRANDEDNESS:
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). 6107060
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                                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTAATTC 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TÁGCCCTGGACTCTGÁTGCTCTGGTCTTCGGTGGACATGGAAGAGTTGGCCACGACGTGG 2176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Greenlee, Winner and Sullivan, P.C.
5370 Manhattan Circle
                                                                                             mat_peptide
191..2467
                                                                                                                                                                                                                                                                 not relevant
                                                              CDS
                                                                                                                                               transit_peptide 2..190
                                                2..2470
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4.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                             28,547
                                                                                                                                                                                                                                                                                                                                                  16:
                                                                                                                                                                                                                                                                                                                                                                                                                   89-97
Score 58.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version
DB 3;
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Length 2763;
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Query Match

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US-09-257-894-12
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                                                   i LOCATION:
US-09-257-894-12
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hubbard, Natalle L.
APPLICANT: Lightner, Jonathan
TITLE OF INVENTION: No. 637674
TITLE OF INVENTION: Expression
TITLE OF INVENTION:
                                                                                                                                                                                                                             TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                          OPOLOGY:
                                                                                                                                                                                                                                                                ELEPHONE:
                                                                                                                                                                                           ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATECTTECCTTTCATTETCCACCCTTCACCAGTAGGGTTAGTGGGGGGCTTCTACAACT 480
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1007 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Broglie, Karu.
Vlein, Theodore M.
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                                                                                                                                          linear
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                                                                                                                                                          single
 4.3%;
56.9%;
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No. 6376749el
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 Score
Pred.
 58.4; DB 4;
No. 3.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Starches via Modification of Starch Biosynthesis
                Length 2772;
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US-09-257-894-2/c
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US-09-257-894-2
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ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
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                                                                Query Match 4.1%;
Best Local Similarity 80.2%;
Matches 65; Conservative
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APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 637674981 Starches via Modification of TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
APPLICATION NUMBER: 09/091,052
APPLICATION NUMBER: 09/091,052
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: 8B-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                                      TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
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OTTY: Wilmington
                                                                                                                                                                                                              LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                              TOPOLOGY:
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348 GTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGACTACCGTGTTTGGGTGTTCCAAGCCT
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    E. I. du Pont de Nemours and Company
1007 Market Street

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                                                                                                                                                                        DNA (genomic)
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                                                                Score 55.4; DB 4;
Pred. No. 8.1e-08;
0; Mismatches 16;
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                                                                                                        Length 414;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/104,158
FILING DATE: 11-AUG-1993
CLASSIFICATION NUMBER: EP PCT/EP92/00302
PRIOR APPLICATION NUMBER: EP PCT/EP92/00302
FILING DATE: 11-FEB-1992
PRIOR APPLICATION NUMBER: BP 921/EP92/00302
FILING DATE: 11-FEB-1992
PRIOR APPLICATION NUMBER: BP 41 04 782.6
FILING DATE: 13-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENEZC/DOCKET NUMBER: FA-1996 PCT (951-91)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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US-08-104-158-1
                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 212-382-0700
TELEFAX: 212-382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2909 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08104158
Patent No. 6215042
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APPLICANT: Willmi
                                                                                                                                                                                               MOLECULE TYPE: C
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sola
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jacobsen, Evert
APPLICANT: Jacobsen, Evert
TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT
TITLE OF INVENTION: CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE
TITLE OF INVENTION: CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
TITLE OF INVENTION: AND PLANTS CONTAINING THESE PLASMIDS
                                                           TISSUE TYPE: tuber
CELL TYPE: total tuber
IMMEDIATE SOURCE:
LIBRARY: CDNA of total
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 10036-8403
                                                                                                                            STRAIN: Desiree
DEVELOPMENTAL STAGE:
TISSUE TYPE: tuber
                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGAAGTACAAGGTATGCTTG 428
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Sonnewald, Jens
Kossmann, Jens
Mueller-Roeber, Bernd
Visser, Richard Gerardus Francisus
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CDS
2..1699
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                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                        growing
                                                                     tuber mRNA in
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SEQ ID NO 1

LENGTH: 2909

TYPE: DNA

ORGANISM: Solanum tuberosum

FEATURE:

NAME/KEY: CDS

LOCATION: (2)...(1699)

OTHER INFORMATION: BRANCHING ENZYME

US-09-609-040-1
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US-09-609-040-1
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Search completed: April 10, 2004, 14:13:17 Job time : 100.567 secs
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APPLICANT: Willmitzer, et al.
TITLE OF INVENTION: NUCLECTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRATE
TITLE OF INVENTION: CONCENTRATION AND COMPOSITION IN PLANTS
FILE REFERENCE: 514413-3515.1
CURRENT APPLICATION NUMBER: US/09/609,040
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US/09/60302
PRIOR APPLICATION NUMBER: PCT/EP92/00302
PRIOR FILING DATE: 1992-02-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
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Best Local Similarity 58.9%;
Matches 93; Conservative
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93; Conservative
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(partial) truncated protein; 97,11 % identity to
active potato branching enzyme"
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Pred. No. 8.6e-07;
0; Mismatches 65
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2: /cgn2-6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2-6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

4: /cgn2-6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2-6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

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11: /cgn2-6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

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14: /cgn2-6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

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16: /cgn2-6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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2 US-10-260-238-3410

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1 US-10-260-238-5563

2 US-10-434-893A-2

2 US-10-434-893A-2

1 US-09-791-149-955

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Sequence 3, Appli
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Sequence 5563, Ap
Sequence 1077, Ap
Sequence 955, App
Sequence 872, App
Sequence 872, App
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equence 14106,	equence 14106,	equence 54140,	equence 54140,	equence	equence 27656,	equence 25407,	equence 1, App1	equence 141092,	equence 1616, A	equence 135	equence 92, App	equence 107, Ap	equence 30, App	quence 2148, Ap	Sequence 442, Ap	equence 36, App	equence 2, Appl	equence 321/2,	equence 33	quence 337, App	equence 264, Ap	equence 14, App	equence 12, Ag	equence 18, App	eguence I, Appi	equence 19, App	equence 16, App	quence 3,	equence 130849,

ALIGNMENTS

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; OTHER INFORMATION: SSBEIIa gene US-10-434-893A-3
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Publication No. US20040060083A1
GENERAL INFORMATION:
APPLICANT: Ahmed Regina
APPLICANT: Matthew Kennedy Morell
APPLICANT: Sadequr Rahman
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and
TITLE OF INVENTION: containing products with an increased amylose content
FILE REFERENCE: 69425
CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 2:1
                                                                                                                                                  Query Match
Best Local Similarity 99.9
Matches 1344; Conservative
                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Aegilops tauschii
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(11476)
OTHER INFORMATION: n is a, c, g o;
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GGGTATGTCACTGGTTTGTCTTTGTTGCATAACAAGTCACAGTTTTAACGTCAGTCTCTTC
                                                            TAGATATCGTGGTATGCAAGAGTTCGATCAGGCAATGCAGCATCTTGAGGAAAAATATG
                                                                                                      TTAGATATCGTGGTATGCAAGAGTTCGATCAGGCAATGCAGCATCTTGAGGAAAAATATG
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GGGTATGTCACTGGTTTGTCTTTGTTGCATAACAAGTCACAGTTTAACGTCAGTCTCTTC

Db 1027 CTGAACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG 1	Db 11272 GCGCCATGACTGGGAGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGCAGATGGATA 11331	
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1141 CGCCATGACTGGGAGGGGATCGTGCCTTTCCCCAGATGCCAGAGGAGGAGCAGATCGATAG	CTTACARAGTAAGAACCAGCAGGGCTIGITKO 	O U D
QY 1081 CTCCAGAGAGCTCGTGGATCGTGAGCGAAGCGACGGGCAACGGCGCGAGGCTGCTCCAAG 1	960 GGAACATCCGCATGACAACAGGCCGCGCTTCTTCGGGTGTACACTCCGAGCAGAACTGC 101	. U .O
OY 1021 GTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCGGCTTGTTACAAGGCAAAGAGAGA 1	00 TCGTCTTGACTCAACTGCTTACAAATCTGAATCAACTTCCCAATTGCTGATGCCCTTGCA 959 11 1 1 1 1 1 1 1 1	9 0
QY 961 GAACATCCGCATGACAACAGGCCGCGCTCTTTCTCGGTGTACACTCCGAGCAGAACTGCG 1	TAAGTCTGGGCTCAAGCGTCACTTGAC 8	ט ט
Query Match 27.5%; Score 370; DB 15; Length 1119; Best Local Similarity 100.0%; Pred. No. 3.8e-105; Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps	A — A	ם ס
; LENGTH: 1119 ; TYPE: DM: ; ORGANISM: Triticum aestivum US-10-260-238-3410	GTTTC 7	υю
; PRIOR APPLICATION NUMBER: US 60/370,620 ; PRIOR FILING DATE: 2002-04-04 ; NUMBER OF SEQ ID NOS: 6077 ; SEQ ID NO 3410	QY 660 GCTCAGTTGGACTCGGTCTAATACTAGAACTATTTCCGAATCTACCCTAACCATCCTAG 719	ט ט
; PRIOR APPLICATION NUMBER: US 60/325,448 ; PRIOR FILING DATE: 2001-09-26 ; PRIOR APPLICATION NUMBER: US 60/325,277 ; PRIOR FILING DATE: 2001-09-26	QY 600 GCCCGAAGCACATACCATTCATTCATATTATCTACTTAAGTGTTTGATGTTTAATCTTAAT 659	g Q
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION ; FILE REFERENCE: 60111-NP ; CURRENT APPLICATION NUMBER: US/10/260,238 ; CURRENT FILING DATE: 2002-09-26	A - 5	g ø
	TAGGGT 53	<u> </u>
79 ; APPLICANT: Cooper, Bret , APPLICANT: Glazebrook, Jane)611 ; APPLICANT: Goff, Stephen A. , APPLICANT: Katagiri, Fumiyaki	Qy 420 GTATGCTTGCCTTTCATTGTCCACCCTTCACCAGGTAGGGTTAGTGGGGGCTTCTACAAC 479	D 10
GENERAL INFORMATION: APPLICANT: Budworth, Paul R. APPLICANT: Bridgs, Steven P.	Qy 360 CACTGGAGCAATAGCTTTTTTGACTACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAG 419	ā ið
RESULT 2 US-10-260-238-3410 ; Sequence 3410, Application US/10260238 ; Publication No. US20040016025A1	301 ATGAGGAAGATAAGGTGATCATCCTC-AAAAGAGGAGATITTGGTATTTGTTTTCAACTTC 35 	망양
Db 11452 GCCCGTGCGCTCAACGTGAAAATCC 11476	241 CAGCACTGACAATGTAACTGCAGTTTATGACATCTGAGCACCAGTATGTTTCACGGAAAC 30	8 8
11392	181 AGCTGGAATTGCTTTTCACCAAAACTATTTTCTTAAGTGCTTGTGTATTGATACATATAC 240	ρ γ _δ
Qy 1200 GGTAGCTTGTTGGTGAGCGCTCGAAGAAAATGGACGGGCCTGGGTGTTTGTT	y 121 AAGTGGTAAAAAAGTGTAGAATTAATTCCTGTAATGAGATGAAAACTGTGCAAAGGCGG 180 	Db Qy

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ghamer, Todd G.

ggs, Steven P.

per, Bret
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E, Stephen A.
agiri, Fumiyaki
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                                                                                                                                        TGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGCAGATGGATAG
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RESULT 3
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US-09-792-127-1
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APPLICANT: Ahmed Regina
APPLICANT: Ahmed Regina
APPLICANT: Matthew Kennedy Morell
APPLICANT: Sadequr Rahman
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch.
TITLE OF INVENTION: containing products with an increased amylose content
FILE REFERENCE: 69425
CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT APPLICATION TOWNSER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 2.1
                                                                                                                           Sequence 1, Application US/09792127 Patent No. US20020002713A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 343; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
LENGTH: 2554
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APPLICANT: Beckles, Diane M.
APPLICANT: Butler, Karla
APPLICANT: Pearlstein, Rich
TITLE OF INVENTION: Starch Branching Enzyme IIb
FILE REFERENCE: BB1439 US NA
                                                         APPLICANT: Allen, Steve
APPLICANT: Beckles, Dian
APPLICANT: Butler, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Hordeum vulgare
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Patent No. US20020002713A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Beckles, Diane M.
APPLICANT: Butler, Karla
APPLICANT: Bettler, Rich
TITLE OF INVENTION: Starch Branching
THE REFERENCE: BB1439 US NA
CURRENT PELICATION NUMBER: US/09/79;
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/186098
PRIOR FILING DATE: 2000-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/792,12
CURRENT FILING DATE: 2001-02-23
CURRENT FILING DATE: 2001-03-01
FRIOR FILING DATE: 2000-03-01
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 2559
TYPE: DNA
ORGANISM: Triticum aestivum
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SEQ ID NO 3
LENGTH: 3039
TYPE: DNA
ORGANISM: Triticum aestivum
US-09-792-127-3
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Best Local Similarity 78.9%;
Matches 146; Conservative
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Best Local S
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Local Similarity 78.9%;
nes 146; Conservative
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                                                                                                                                    2316 TTTGAAAAAGGGGACTTGGTATTTGTGTTCAACTTCCACTGGAGTAGTAGCTATTTCGAC
                                                                                                                                                                                                                  2256 TTTATGACATCAGACCACCAGTACGTATCTCGGAAACATGAGGAAGATAAGGTGATCGTG 2315
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                                                                           TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTTTGCCTTTTCATTGTCCA 443
                                                                                                                                                             CTCAAAAGAGGGAGAITTGGTAITTGTTTTCAACTICCACTGGAGCAATAGCTITTTTTGAC 383
      CCCTT 448
                                              TACCGGGTCGGCTGTTTAAAGCCTGGGAAGTACAAGGTGGTCTTAGACTCGGACGCTGGA
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                                                                                                                                                                                                                                                                                                    Score 122.6; DB 9;
Pred. No. 6.5e-27;
0; Mismatches 39;
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PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 3480
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Best Local Similarity 84.1%;
Matches 138; Conservative
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                                                                                                                                                                                                               APPLICANT: Budworth, Paul R. APPLICANT: Moughamer, Todd G APPLICANT: Briggs, Steven P. APPLICANT: Cooper, Bret_
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APPLICANT: Moughamer, Todd G.
APPLICANT: Briggg, Steven P.
APPLICANT: Cooper, Bret
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                                      TLE OF INVENTION: PROMOTERS FOR REGULATION OF
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FERENCE: 60111-NP
APPLICATION NUMBER: US/10/260,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTATGACATCAGACCÁCCAGTACGTATCTCGGAAACÁTGÁGGÁÁGATAAGGTGÁTCGTG 572
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Goff, Stephen A.
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Ricke, Darrell
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                                                                                                                                                                 Goff, Stephen A.
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                                                                                    Ricke,
                                                                                                        Provart, Nicholas
                                                                                                                               Kreps, Joel
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                                             PLANT EXPRESSION
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RESULT 9 US-10-260-238-1027

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CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR PRIOR PRIOR DATE: 2001-09-26
PRIOR PPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 5563
LENGTH: 636
TYPE: DNA
ORGANISM: Zea mays
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TYPE: DNA
ORGANISM: Hordeum vulgare
FEATURE:
OTHER INFORMATION: SSBEIID cDNA
US-10-434-893A-2
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APPLICANT: Matthew Kennedy Morell
APPLICANT: Matthew Kennedy Morell
APPLICANT: Sadequr Rahman
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and
TITLE OF INVENTION: containing products with an increased amylose content
FILE REFERENCE: 69425
CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 2.1
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10434893A Publication No. US20040060083A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 138; Conservative
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                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                     , Match 8.9%; Score 119.6; DB 12; Length 2780;
Local Similarity 84.8%; Pred. No. 5.4e-26;
Les 134; Conservative 0; Mismatches 24; Indels 0;
                                                                                                                                                                                            2182
2302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 TCCTCAAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 AATTCATGACATCTGATCACCAGTATATTTCCCGGAAACATGAGGAGGATAAGGTGATTG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTCGAAAAGGGAGATTTGGTATTTGTGTTCAACTTCCACTGCAACAACAACAGCTATTTTG
                                                TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGT 421
                                                                                           TTTGAAAAAGGGGACTTGGTATTTGTGTTCAACTTCCACTGGAGTAATAGCTATTTCGAC
                                                                                                                                           CTCAAAAGGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGAC 383
                                                                                                                                                                                         TTTATGACATCAGACCACCAGTACGTATCTCGGAAAACACGAGGAAGATAAGGTGATCGTG 2241
                                                                                                                                                                                                                                    TTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCATC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTACCGTATTGGTTGTCGAAAGCCTGGGGTGTATAAGGTGGTCTTG
  TACCGGGTCGGTTGCTTAAAGCCTGGGAAGTACAAGGT 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.0%; Score 120.6; DB 1
82.6%; Pred. No. 9.2e-27;
ative 0; Mismatches 29
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GENERAL INFORMATION:

Sequence 1027, Application US/10260238 Publication No. US20040016025A1

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APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT APPLICATION NUMBER: US 60/325,448
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILLING DATE: 2001-09-26
PRIOR FILLING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 1027
LENGTH: 1642
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US-09-770-149-955/c
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; ORGANISM: Oryza sativa
US-10-260-238-1027
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                                                                                                                                                                                                                                                                                                                                         Sequence 955, Application US/09770149 Patent No. US20020059663A1
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1341 TTATATTTGÁGÁAGGGAGATCTGGTATTTGTGTTCAACTTCCATTGGAGTAACAGCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1281 TGGGGTTCATGACATCAGACCACCAGTACATATCTCGAAAGCATGAAGAGGATAAGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGACTACCGTGTTGGTTTTAAAGCCCAGGGAAATATAAGAGGTGGT 1448
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Provart, Nicholas
Ricke, Darrell
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Goff, Stephen A.
                                                                           Garcia, Carlos A.
Kricker, Maja
Slader, Ted
                                                                                                                                                                                                                                                      An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
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             Hoffman, Neil
Hurban, Patrick
                                           Davis, Keith R.
Allen, Keith
                                                                                                                         Woessner, Jeffrey P.
Haas, William David
                                                                                                                                                         Matthew, Abraham V.
Ledford, Brooke L.
                                                                                                                                                                                           Page,
                                                                                                                                                                                                        Yu, Yang
Rameaka, Joshua G.
                                                                                                                                                                                                                                          Raines, Tracy M.
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Expressed Sequences of Arabidopsis
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Pred. No. 3e-22;
0; Mismatches 38;
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US-09-938-842A-872
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                                                                                                                                                                                              US-09-938-842A-872
                                                                                                                                                                                                                           ; SEQ ID NO 872
; LENGTH: 2418
; TYPE: DNA
   2158 TTCGÁAÁGÁGGTGÁTCTCGTCTTTTÁACTTTCACTGGÁCCAGCÁGCTACTTTGÁT 2217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384
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Sequence 872, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
CURLENTON: SAME, AND METHODS OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-06-22

NUMBER: US 60/300,111

PRIOR FILING DATE: 2001-06-22
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CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 955
LENGTH: 602
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; ORGANISM: Arabidopsis thaliana
US-09-770-149-955
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Best Local Similarity
Matches 130; Conserv
                                                                                                                                                                                      Query Match 7.2%; Score 97; DB 9; Le Best Local Similarity 70.3%; Pred. No. 6.4e-19; Matches 130; Conservative 0; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 5379
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                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana
                                                                          2098 TTTATGACTTCGGÁGCACCAATTCATATCACGAAAAGACGAAGCAGATAGAGTAATCGTA 2157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 CTCAAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGAC 383
324 CTCAAAAGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490 TTTATGACTTCGGAGCACCAATTCATATCACGAAAGACGAAGCAGATAGAGTAATCGTA
                                                                                                                               264 TTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCATC 323
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Pred. No. 2.4e-19;
0; Mismatches 55
                                                                                                                                                                                                                                                 Length 2418;
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                                                                                                                                                                                                                                                                                 US-10-056-454A-17
                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                  Sequence 17, Application US/10056454A
Sequence 17, Application US/10056454A
Publication No. US20030166919A1
GENERAL INFORMATION:
GENERAL INFORMATION: Improvements in or Relating to Plant Starch Composition
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
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LENGTH: 2418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER: OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kreps, Joe
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2218
                                                                                                                                                                                                                                                                                                                                                                                      2278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2218
                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2158 TICGAAAGAGGIGAICTCGICTTIGICTTIAACTITCACTGGACCAGCAGCIACTTIGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2098 TTTATGACTTCGGAGCACCAATTCATATCACGAAAAAGACGAAGCAGATAGAGTAATCGTA 2157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCAAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGAC 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTTTGCCTTTTCATTGTCCA 443
                                                                                                                                                                                                                                                                                                                                                                                      CTCTT 2282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACCGCATTGGTTGCTCCAAGCCTGGAAAATATAAGATCGTATTGGACTCGGACGATCCT 2277
                 CITY: Newcastle
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCIT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACCGTGTTGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTTTGCCTTTTCATTGTCCA 443
COUNTRY: United States of America
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Pred. No. 6.4e-19;
0; Mismatches 55; Indels
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ZIP: 19720

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-10-056-454A-13
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                                                                                                                                                                  , SEQUENCE DESCRIPTION: SEQ ID NO: US-10-056-454A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Vers

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/056,454A

FILING DATE: 25-Jun-2002

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/10056454A Publication No. US20030166919A1 GENERAL INFORMATION: National Starch and APPLICANT: National Starch and
Query Match 6.9%; Score 92.6; DB 14; Best Local Similarity 68.4%; Pred. No. 1.8e-17; Matches 128; Conservative 0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 7.1%; Local Similarity 69.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: National Starch and Chemical Investment Holding Corporation TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 AGTITATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAAGATAAGGTGATCA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACCCTT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTATCGCATAGGCTGCCTGAAGCCTGGAAAATACAAGGTTGGCTTGGACTCAGATGATC 2354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTACCGIGITGGGGGTGTTCCAAGCCTGGGAAGTACAAGGTATGCTTGCCTTTTCATTGTC 441
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                  LENGTH: 2975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
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Pred. No. 2.1e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.30
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Search completed: April 10, 2004, 20:07:39 Job time: 478.681 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 8329
LENGTH: 1867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.8%; Score 91.6; DB 12; Length 1867; Best Local Similarity 68.3%; Fred. No. 2.7e-17; Matches 127; Conservative 0; Mismatches 59; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2583 CACTTTT 2589
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                                                                                                            1059 TTGTTC 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 ACTACCGTGTTGGGGTTCCAAGCCTGGGAAGTACAAGGTATGCTTGCCTTTTCATTGTC 441
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                                                                                                                                                                                                                     999 TACAGAGTTGGCTGTTCAACCCCTGGGAAATATAAGATTGTCTTGGATTCAGATGATGCC 1058
                                                                                                                                                                                                                                                                                                                               939 Trogadagegegeaacerearctrierctricaartricatriegaacaacaacactatricagar 998
                                                                                                                                                                                                                                                                                                                                                                               324 CTCAAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTGAC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 TTTATGACATCTGAGCACCAGTATGTTTCACGGAAACATGAGGAAGATAAGGTGATCATC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATTTGAAAGAGGAAACCTAGTTTTCGTCTTTAATTTTCACTGGACAAATAGCTATTCAG 2522
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCATGACTGCTGAGCACCAATATATTTCACGGAAAAATGAAGGTGACAAAATTATAGTC 938
                                                                                                                                                               CCCTTC 449
                                                                                                                                                                                                                                                                   TACCGIGITIGGGIGITICCANGCCIGGGAAGIACAAGGIAIGCITIGCCITITICATIGICCA 443
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Result
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Listing first 45 summaries
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Perfect score:
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  4004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D8
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seq length: 2000000000
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ALIGNMENTS

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DEFINITION 167 wheat seed cDNA library Triticum aestivum cDNA, mRNA sequence.

DEFINITION 167 wheat seed cDNA library Triticum aestivum cDNA, mRNA sequence.

DEFINITION 1607192

VERRICON 180607192.1 GI:23270467

KEYWORDS

Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum (bread wheat)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; poideae; Triticuae;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooldeae; Triticaea; Triticum.

REFERENCE 1 (bases 1 to 724)

Li,J., Wang,F., Li,Q. and Zhang,X.

Expressed sequence tags analysis of a wheat seed cDNA library

COMMENT Contact: Xiansheng Zhang

Plant development molecular biology lab

college of life sciences

Shan dong agriculture university, Tai'an, Shan dong, China

Tel: 086-0538-824114

Email: Zhiwufy@sdau.edu.cn.

Location/Qualifiers

1.724

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Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
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               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
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TaE05016F12F TaE05 Triticum aestivum
      Cloutier, S
                                                                  Triticum aestivum
                                                                               Triticum aestivum (bread
                                                                                                                                                                                                                       CCCGTGCGCT
                                                                                                         GI:20433322
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Genoplante 93, rue Henri Rochefort 91025 EVRY CEDEX France 93, rue Henri Rochefort 91025 EVRY CEDEX France Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Pred. No. 1.4e-97;
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573

mRNA CDNA

clone

linear

r EST 03-MAY-2002 TaE05016F12F, mRNA

wheat)

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TITLE
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Best Local Similarity
Matches 368; Conservat
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Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-2340
Fax: (204) 983-2604
Email: scloutier@agr.gc.ca
was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >2.0 kb
Plate: 016 row: F column: 12
Seq primer: MJ3 Forward.
                                                                                                                                       CK210642 1107 bp mRNA linear EST 08-DEC-2003 FGAS022466 Triticum aestivum FGAS: Library 5 GATE 7 Triticum
Triticum aestivum (bread wheat)
Triticum aestivum
Eukarvota; Viridivlantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                               CK210642.1 GI:39573032
                                                                                                                     aestivum cDNA,
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/dev stage="5 days after anthesis"
/lab_host="E. coli DH1DB"
/clone_lib="TaE05"
/note="Vector: pSPORT-P (Invitrogen Technologies);
NotI, Site_2: MulI; mENA obtained from wheat seeds cultivar Glenlea 5 days post-anthesis"
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1. .573
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/cultivar="Glenlea"
/db_xref="taxon:4565"
/clone="TaE05016F12F"
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/mol_type="mRNA"
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99.5%;
                                                                                                                       mRNA sequence.
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Fax: 306 966 2033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; pooideae; Triticeae; Triticum.

1 (bases 1 to 1107)

Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D., Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A., Links,M.G., McCarthy,E.L., Moncoy,A., Muzak,I., Nilson,D., Penniket,C., Roach,J.L. and Sarhan,F.

Punctional Genomics of Abiotic Stress In Wheat and Canola Crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: fgas ests@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2003)
Contact: Wm L Crosby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the region [18,830].
Plate: L5B023 row: I column: 05.
Location/Qualifiers
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//organism="Triticum aestivum"
//db xref="taxon:4565"
//done lib="Triticum aestivum FGAS: Library 5 GATE 7"
//done lib="Triticum aestivum Activar Norstar. 4 mRNA
of spike formation in wheat cultivar Norstar. 4 mRNA
of spike formation in from lcm crown sections after
10 days of cold accilmation. The second is from lcm crown
10 days of cold accilmation. The second is from lcm crown
11 deaccilmation plants were fully vernalized for 49 days).
12 The third is from different developmental stages of spike
13 formation (5 to 50mm) that still have not emerged from the
14 leaf (dissection required). The last is from different
15 developmental stages of spike and seed formation after
16 having emerged from the leaf (visible). First strand
17 synthesis in this library was done in the presence of
18 methylated dCTP thereby protecting from internal cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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(bases 1 to 447)

I (bases 1 to 447)

Zhang, D., Klueva, N., Barker, G.L.A., Wilson, I.D., Edwards, K.J., Close, T.J., Zheng, H., McCartor, K., Soares, B.M. and Nguyen, H.T. Combining expressed-sequence-tags sequencing and subtractive hybridization for rapid identification of differentially express genes under heat stress in wheat (Triticum aestivum (L.) Moench) Unpublished (2003)

Contact: Barker GL.
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AJ604482 T07
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University of Bristol
Woodland Road Bristol
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
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CCCGTGCGCTCAACGTGAAAAT 1342
                                                                                                                               CTGAACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG 1320
                                                                                  CT--ACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG
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nilarity 98.4%;
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/mol_type="mRNA"
/culfivar="Mustang"
/db_xref="taxon:4565"
/clone="H12_T07_plate_9"
/tissue_type="Heat stressed whole seedlings"
/dev_stage="2_weeks_old"
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Triticum aestivum cDNA clone H12_T07_plate_9, mRNA
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Pred. No. 3.7e-95;
0; Mismatches 4
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   44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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G118.114J06R010926 G118 Triticum aestivum cDNA clone
mRNA sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Pooideae; Triticeae; Triticum.
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Unpublished (2003)
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                                                                            CTGAACCCTCCTATCTTGCACATTCCCGGGTTGTTTTGTACATATAACTAATAATTG 1320
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 CCCGTGCGCTCAACGTGAACAT
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larity 98.4%;
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                                                          ACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol type="mRNA"
/cultivar="recital"
/db_xref="taxon:4565"
/clone="G118114J06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="grain (118 pollination)"
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Pred. No. 4.2e-95;
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CCCGTGCGCTCAACGTGAACAT

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Fax: (204) 983-4604
Email: scloutier@agr.gc.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average insert size is 3.1.4 kb
Plate: 032 row: A column: 02
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Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
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405 bp mRNA linear EST 03-MAY-2002
TaE15032A02F TaE15 Triticum aestivum cDNA clone TaE15032A02F, mRNA
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                                                                                                       CTGAACCCTCCTCCTATCTTGCACATTCCCCGGTTGTTTTTTGTACATATAACTAATAATTG 1320
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/dev_stage="15 days after anthesis"
/dev_stage="15 days after anthesis"
/lab_host="8. coli DHIOB"
/clome_lib="Tas15"
/clome_lib="Tas15"
/clome_type="Tas15"
/clome_type="Tas15
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Pred. No. 8.1e-95;
0; Mismatches 6
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G118.127M24F010824 G118
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been 9
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Unpublished (2003)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 692)
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                   CCCGTGCGCTCAACGTGAAAAT 1342
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/cultivar="recital"
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1 (bases 1 to 414)
1 (bases 1 to 414)
1 (Ogihara, Y. and Murai, K.
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
Tel: 81-559-81-6856
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Location/Qualifiers
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/dev_stage="Feekes' scale 10.5"
/clone_lib="Y. Ogihara unpublished cDNA library,
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/cultivar="Chinese Spring"
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/clone="whoh9k12"
491 bp mRNA linear Ogihara unpublished cDNA library, Wh_e
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ACCESSION VERSION KEYWORDS

mRNA sequence. CK153053 CK153053.1 GI: EST.

GI:38972724

LOCUS DEFINITION RESULT 11 CK153053/c

CK153053 FGAS031606 Triticum

897 n aestivum

FGAS:

mRNA linear EST 05-DEC-2 Talt2 Triticum aestivum cDNA,

EST 05-DEC-2003

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1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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Contact: Tadasu Shin-i
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Ogihara, Y. and Murai, K.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Location/Qualifiers
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                                                                        CTGAACCCTCCTATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG 1320
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                                                                                                                                                                                                                                                           CTCCAGAGAGCTCGTGGATCGTGAGCGAAGCGACGGCGAAGCGAGGCTGCTCCAAG 1140
                                                                                                                                                                                                                                                                                                GTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCGCTTGTTACAAGGCAAAGAGAGAA
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                          CCCGTGCGCTCAACGTGAAAAT
                                                                                                                  CGCCATGACTGGGAGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGCAGATGGATAG
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   CCCGTGCGCTCAACATGAACAT
                                                         CT--ACCCTCATATCTTGCACATTCCCGGTTGTTTTTGTACATATAACTAATAATTG
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/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="seed DPA10"
/dev_stage="Feekes' scale 11.2"
/clone_lib="Y. Ogihara unpublished cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="whe11m24"
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Pred. No. 3.4e-94;
0; Mismatches 6
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Best Local Similarity
Matches 374; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: fgas_ests@cs.usask.ca
This sequence is the direct result of the
phred (default parameters). It is the raw
identification of the high quality insert
(default parameters) has been run on this
the region [125.627].
Plate: Talt237 row: A column: 20.
Location/Qualifiers
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University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Tel: 306 966 2033
Tesai: 306 966 2033
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1 (bases 1 to 897)

Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,I Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,I Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A., Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D., Penniket,C., Roach,J.L. and Sarhan,F.

Functional Genomics of Abiotic Stress In Wheat and Canola Crops Unpublished (2003)

Contact: Wm.L. Crosby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triticum aestivum (bread wheat)
Triticum aestivum
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
CCCGTGCGCTCAACGTGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCGTGTATGCCCTTACAGAGTAAGAACCAGCAGCGGCTTGTTACAAGGCAAAGAGAGAA 1080
                                                                                                                                                                                                                                                                                  CGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCAGATGCCAGGAGGAGGAGATGGATAG 1200
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                                                                                                         GTCGTGTATGCCCCTACAGAGTAAGAACCAGCAGCTGCTTGTTACAAGGCAAAGAGAGAA
                                                                                                                                                                                                                                            CGCCATGACTGGGAGGGGATCGTGCCTCTTCCCCCAGATGCCAGGAGGAGCAGATGGATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="Triticum aestivum FGAS: Tait2"
/note="Organ: Crown; Vector: pGEM-T; SSH (suppression subtractive hybridization) cDNA library from genotype CI14106 cold hardened at 2 C for 1 day (24 H) (tester) as subtractive against genotype Norstar cold hardened at 2 c for 21 days and 49 days (equal amount of cDNA pooled together before subtraction, driver). Nitro-pyrole anchored oligo-dT priming and non-directional cloning."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/cultivar="Wheat line CI 14106"
/db_xref="tcaxon:4565"
/lab_host="DHS alpha"
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                           1342
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Best Local Similarity
Matches 370; Conserva
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Triticum aestivum
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BJ273375 C. Ogihara unpublished cDNA library, Whoh Triticum aestivum cDNA clone whoh16p06 3', mRNA sequence.
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Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
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Location/Qualifiers
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                                                                                                              CCCGTGCGCTCAACGTGAAA 1340
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/dev_stage="Feekes' scale 10.5"
/clone_lib="Y. Ogihara unpublished cDNA library,
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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CD899313
G174.111021F010825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93, rue Henri Rochefort 91025 EVRY CEDEX France Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the fren plant genomics programme 'Genoplante' (http://www.genoplante.and http://genoplante.info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticaea; Triticum.

1 (bases 1 to 527)
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CD934119
CD934119.1 GI:32781883
EST.
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GR45.123A24F010723 GR45 Triticum aestivum cDNA clone
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Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="grain
pollination)"
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/cultivar="recital"
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/clone="GR45123A24"
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96.2%;
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mRNA sequence.
CD897227
CD897227.1 GI:32671
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plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Tel: 33 1 69 47 54 00
Teax: 33 1 69 47 54 10
This sequence has been g
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Unpublished (2003)
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1 (bases 1 to 532)
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Triticum aestivum
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pollination)"
/clone_lib="G174"
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/clone="G174111021"
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/cultivar="recital"
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Triticum aestivum
Eukaryota; Viiidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 565)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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pollination)"
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/mol_type="mRNA"
/cultivar="recital"
/db_xref="taxon:4565"
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/clone="G174105D15"
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